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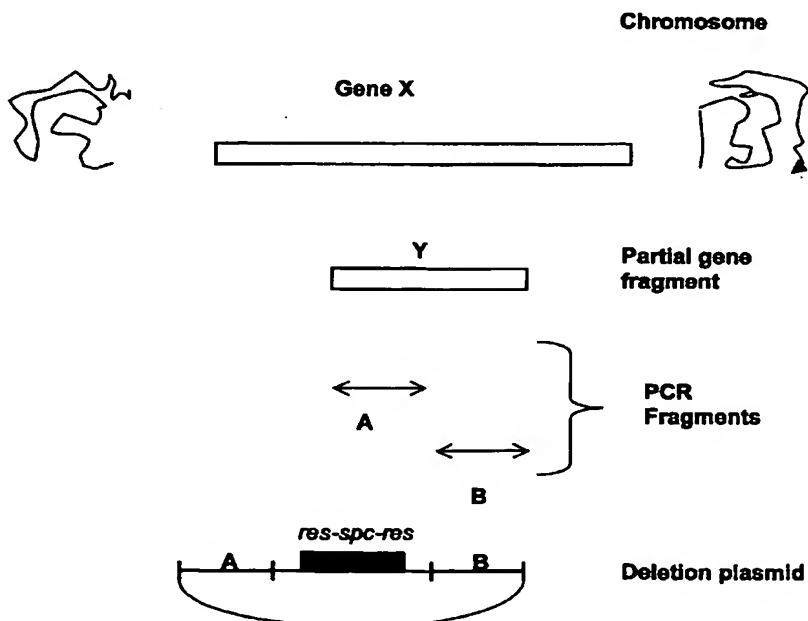
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(54) Title: METHODS FOR MONITORING MULTIPLE GENE EXPRESSION

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(57) Abstract: The present invention relates to methods for monitoring differential expression of a plurality of genes in a first *Bacillus* cell relative to expression of the same genes in one or more second *Bacillus* cells using microarrays containing *Bacillus* genomic sequenced tags. The present invention also relates to computer readable media and computer-based systems. The present invention further relates to substrates containing an array of *Bacillus licheniformis* or *Bacillus clausii* GSTs.



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METHODS FOR MONITORING MULTIPLE GENE EXPRESSION**Background of the Invention**

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Field of the Invention

The present invention relates to methods for monitoring expression of a plurality of genes in *Bacillus* cells. The present invention also relates to *Bacillus* genomic sequenced tags and to substrates and computer readable media containing such genomic 10 sequenced tags.

Description of the Related Art

Microarray technology is increasingly becoming the method of choice for the quantitative and simultaneous analysis of the expression levels of many thousands of 15 genes. Microarray analyses typically follow the steps of gene selection, microarray synthesis, sample preparation, array hybridization, detection, and data analysis (Watson *et al.*, 1998, *Current Opinion in Biotechnology* 9: 609-614).

PCR-amplified coding sequences of genomic DNA from an organism are particularly useful in microarrays for obtaining global expression profiles where the 20 genome of the organism has been fully sequenced.

Chu *et al.*, 1998, *Science* 282: 699-705 disclose the use of microarrays containing PCR-amplified genomic coding sequences for determining the temporal expression of *Saccharomyces cerevisiae* genes during sporulation.

For other organisms whose genomes have not been sequenced, global expression 25 profiles may be obtained with arraying (1) random genomic DNA segments or clones (e.g., from a genomic DNA library); (2) random cDNA clones (e.g., from one or more cDNA libraries) that are uncharacterized at the DNA sequence level; or (3) random cDNA clones that have been sequenced and partially characterized with respect to putative identification and function.

30 Genomic sequenced tags (GSTs) are partial genomic DNA sequences. Simply stated, a GST is a segment of a sequence from a random genomic DNA clone that corresponds to part of a specific gene. The use of sequenced GSTs in microarrays compared to genomic clones or random cDNA clones provides several advantages

especially for organisms whose genomes have not been fully sequenced. First, since sequence information is available, redundancy and follow-up characterization is minimized. Second, GST microarrays can be organized based on function of the gene products to facilitate analysis of the results (e.g., GSTs encoding enzymes from the same 5 metabolic pathway can be arranged or grouped accordingly).

Ruan *et al.*, 1998, *The Plant Journal* 15: 821-833, disclose the use of microarrays containing *Arabidopsis thaliana* EST sequences for determining the temporal expression of *Arabidopsis thaliana* genes in root, leaf, and two stages of floral development.

Iyer *et al.*, 1999, *Science* 283; 83-87, disclose the use of microarrays containing 10 human EST sequences for determining the temporal expression of human fibroblast cells in response to serum.

Hayward *et al.*, 2000, *Molecular Microbiology* 35: 6-14, disclose shotgun DNA microarrays and stage-specific gene expression in *Plasmodium falciparum* malaria.

Bacteria are used as host microorganisms for the industrial production of enzymes 15 and other proteins whether endogenous or heterogenous to the microorganisms. There is a need in the art to provide methods for monitoring the global expression of genes from *Bacillus* cells to improve the production potential of these microorganisms.

It is an object of the present invention to provide alternative methods for monitoring expression of a plurality of genes in *Bacillus* cells.

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Summary of the Invention

The present invention relates to methods for monitoring differential expression of a plurality of genes in a first *Bacillus* cell relative to expression of the same or similar 25 genes in one or more second *Bacillus* cells, comprising:

- (a) adding a mixture of labeled nucleic acid probes isolated from the *Bacillus* cells to a substrate containing an array of *Bacillus* GSTs under conditions where the nucleic acids hybridize to complementary sequences of the *Bacillus* GSTs in the array, wherein the nucleic acids from the first *Bacillus* cell and the one or more second *Bacillus* 30 cells are labeled with a first reporter and one or more different second reporters, respectively; and
- (b) examining the array under conditions wherein the relative expression of the

genes in the *Bacillus* cells is determined by the observed hybridization reporter signal of each spot in the array in which (i) the *Bacillus* GSTs in the array that hybridize to the nucleic acids obtained from either the first or the one or more second *Bacillus* cells produce a distinct first hybridization reporter signal or one or more second hybridization reporter signals, respectively, and (ii) the GSTs in the array that hybridize to the nucleic acids obtained from both the first and one or more second *Bacillus* cells produce a distinct combined hybridization reporter signal. In a preferred embodiment, the *Bacillus* GSTs are the *Bacillus licheniformis* GSTs of SEQ ID NOs. 1-4448. In another preferred embodiment, the *Bacillus* GSTs are the *Bacillus clausii* GSTs of SEQ ID NOs. 4449-10 8481.

The present invention also relates to computer readable media, substrates containing an array of *Bacillus* GSTs, and computer-based systems.

Brief Description of the Figure

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Figure 1 shows a method to make deletions at specific loci of the *Bacillus licheniformis* or *Bacillus clausii* chromosome utilizing the *Bacillus licheniformis* or *Bacillus clausii* GST sequences described herein.

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Detailed Description of the Invention

The present invention relates to methods for monitoring differential expression of a plurality of genes in a first *Bacillus* cell relative to expression of the same genes in one or more second *Bacillus* cells. The methods comprise (a) adding a mixture of labeled nucleic acid probes isolated from two or more *Bacillus* cells in culture to a substrate containing an array of *Bacillus* GSTs under conditions where the nucleic acids hybridize to complementary sequences of the *Bacillus* GSTs in the array; and (b) examining the array under conditions wherein the relative expression of the genes in the two or more cells is determined by the observed hybridization reporter signal of each spot in the array.

30 The methods of the present invention may be used to monitor global expression of a plurality of genes from a *Bacillus* cell, discover new genes, identify possible functions of unknown open reading frames, and monitor gene copy number variation and

stability. For example, the global view of changes in expression of genes may be used to provide a picture of the way in which *Bacillus* cells adapt to changes in culture conditions, environmental stress, or other physiological provocation. Other possibilities for monitoring global expression include spore morphogenesis, recombination, metabolic 5 or catabolic pathway engineering.

The methods of the present invention are particularly advantageous when one spot on an array equals one gene or open reading frame because extensive follow-up characterization is unnecessary since sequence information is available, and *Bacillus* GST microarrays can be organized based on function of the gene products. However, 10 one spot may contain more than one gene especially if random genomic sequences are used.

Genomic Sequenced Tags

The term "genomic sequenced tag" or "GST" is defined herein as a segment of a 15 sequence from a random genomic DNA clone of an expressed *Bacillus* genome. The term "GST" will be understood to also include two or more *Bacillus* GSTs assembled into a contig. *Bacillus* GSTs are generally generated as follows: Total cellular DNA is isolated from a *Bacillus* cell, digested with a restriction endonuclease or cleaved by sonication, nebulization, or physical methods, size-selected by agarose gel 20 electrophoresis, isolated, and ligated into a vector, e.g., pSGMU2 (Errington, 1986, *Journal of General Microbiology* 132: 2953-2961). The ligation mixture is used to transform competent *E. coli* cells and transformants are selected under selective pressure, e.g., ampicillin selection. Plasmids from the genomic DNA libraries are generated from 25 random selected transformants, isolated, and partially sequenced. The partial sequences are then compared to sequences in various publicly available databases, for example GenBank, EMBL, Swissprot etc., for identification of function and annotated accordingly.

In the methods of the present invention, the *Bacillus* GSTs are preferably at least about 50 bp in length, more preferably at least about 100 bp in length, even more 30 preferably at least about 150 bp in length, and most preferably at least about 200 bp in length.

The *Bacillus* GSTs may be obtained from any *Bacillus* cell but preferably from a

Bacillus alkalophilus, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus laetus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, or *Bacillus thuringiensis* cells. In a preferred embodiment, the 5 *Bacillus* cell is a *Bacillus clausii* cell.

In a preferred embodiment, the *Bacillus* GSTs are obtained from a *Bacillus licheniformis* cell. In a more preferred embodiment, the *Bacillus licheniformis* GSTs are obtained from *Bacillus licheniformis* ATCC 14580. In a most preferred embodiment, the 10 *Bacillus licheniformis* GSTs are selected from the group consisting of SEQ ID NOs. 1-4448, nucleic acid fragments of SEQ ID NOs. 1-4448, and nucleic acid sequences having at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 1-4448.

In another preferred embodiment, the *Bacillus* GSTs are obtained from a *Bacillus clausii* cell. In another more preferred embodiment, the *Bacillus clausii* GSTs are 15 obtained from *Bacillus clausii* NCIB 10309. In another most preferred embodiment, the *Bacillus clausii* GSTs are selected from the group consisting of SEQ ID NOs. 4449-8481, nucleic acid fragments of SEQ ID NOs. 4449-8481, and nucleic acid sequences having at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 4449-8481.

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Microarrays

The term "an array of *Bacillus* GSTs" is defined herein as a linear or two-dimensional array of preferably discrete elements of *Bacillus* GSTs, each having a finite area, formed on the surface of a solid support.

25 The term "microarray" is defined herein as an array of *Bacillus* GST elements having a density of discrete GST elements of at least about 100/cm², and preferably at least about 1000/cm². The GST elements in a microarray have typical dimensions, e.g., diameters, in the range of between about 10 to about 250 μ m, preferably in the range of between about 10 to about 200 μ m, more preferably in the range of between about 20 to 30 about 150 μ m, even more preferably in the range of between about 20 to about 100 μ m, most preferably in the range of between about 50 to about 100 μ m, and even most preferably in the range of between about 80 to about 100 μ m, and are separated from

other GST elements in the microarray by about the same distance.

Methods and instruments for forming microarrays on the surface of a solid support are well known in the art. See, for example, U.S. Patent No. 5,807,522; U.S. Patent No. 5,700,637; and U.S. Patent No. 5,770,151. The instrument may be an 5 automated device such as described in U.S. Patent No. 5,807,522.

The term "a substrate containing an array of *Bacillus* GSTs" is defined herein as a solid support having deposited on the surface of the support one or more of a plurality of *Bacillus* GSTs for use in detecting binding of labeled nucleic acids to the *Bacillus* GSTs.

The substrate may, in one aspect, be a glass support (e.g., glass slide) having a 10 hydrophilic or hydrophobic coating on the surface of the support, and an array of distinct *Bacillus* GSTs bound to the coating, where each distinct GST is disposed at a separate, defined position.

Each microarray in the substrate preferably contains at least 10^3 distinct *Bacillus* 15 GSTs in a surface area of less than about 5 or 6 cm^2 . Each distinct *Bacillus* GST (i) is disposed at a separate, defined position in the array, (ii) has a length of at least 50 bp, and (iii) is present in a defined amount between about 0.1 femtomoles and 100 nanomoles or higher if necessary.

For a hydrophilic coating, the glass slide is coated by placing a film of a 20 polycationic polymer with a uniform thickness on the surface of the slide and drying the film to form a dried coating. The amount of polycationic polymer added should be sufficient to form at least a monolayer of polymers on the glass surface. The polymer film is bound to the surface via electrostatic binding between negative silyl-OH groups on the surface and charged cationic groups in the polymers. Such polycationic polymers include, but are not limited to, polylysine and polyarginine.

25 Another coating strategy employs reactive aldehydes to couple DNA to the slides (Schena *et al.*, 1996, *Proceedings of the National Academy of Science USA* 93: 10614-10619; Heller *et al.*, 1997, *Proceedings of the National Academy of Science USA* 94: 2150-2155).

30 Alternatively, the surface may have a relatively hydrophobic character, *i.e.*, one that causes aqueous medium deposited on the surface to bead. A variety of known hydrophobic polymers, such as polystyrene, polypropylene, or polyethylene, have desirable hydrophobic properties, as do glass and a variety of lubricant or other

hydrophobic films that may be applied to the support surface. A support surface is "hydrophobic" if an aqueous droplet applied to the surface does not spread out substantially beyond the area size of the applied droplet, wherein the surface acts to prevent spreading of the droplet applied to the surface by hydrophobic interaction with the droplet.

In another aspect, the substrate may be a multi-cell substrate where each cell contains a microarray of *Bacillus* GSTs, and preferably an identical microarray, formed on a porous surface. For example, a 96-cell array may typically have array dimensions between about 12 and 244 mm in width and 8 and 400 mm in length, with the cells in the array having width and length dimension of 1/12 and 1/8 the array width and length dimensions, respectively, *i.e.*, between about 1 and 20 in width and 1 and 50 mm in length.

The solid support may include a water-impermeable backing such as a glass slide or rigid polymer sheet, or other non-porous material. Formed on the surface of the backing is a water-permeable film which is formed of porous material. Such porous materials include, but are not limited to, nitrocellulose membrane nylon, polypropylene, and polyvinylidene difluoride (PVDF) polymer. The thickness of the film is preferably between about 10 and 1000 μm . The film may be applied to the backing by spraying or coating, or by applying a preformed membrane to the backing.

Alternatively, the solid support may be simply a filter composed of nitrocellulose, nylon, polypropylene, or polyvinylidene difluoride (PVDF) polymer, or for that matter any material suitable for use.

The film surface may be partitioned into a desirable array of cells by water-impermeable grid lines typically at a distance of about 100 to 2000 μm above the film surface. The grid lines can be formed on the surface of the film by laying down an uncured flowable resin or elastomer solution in an array grid, allowing the material to infiltrate the porous film down to the backing, and then curing the grid lines to form the cell-array substrate.

The barrier material of the grid lines may be a flowable silicone, wax-based material, thermoset material (*e.g.*, epoxy), or any other useful material. The grid lines may be applied to the solid support using a narrow syringe, printing techniques, heat-seal stamping, or any other useful method known in the art.

Each well preferably contains a microarray of distinct *Bacillus* GSTs. "Distinct *Bacillus* GSTs" as applied to the GSTs forming a microarray is defined herein as an array member which is distinct from other array members on the basis of a different GST sequence, and/or different concentrations of the same or distinct GSTs, and/or different mixtures of distinct GSTs or different-concentrations of GSTs. Thus an array of "distinct *Bacillus* GSTs" may be an array containing, as its members, (i) distinct GSTs, which may have a defined amount in each member, (ii) different, graded concentrations of given-sequence GSTs, and/or (iii) different-composition mixtures of two or more distinct GSTs.

10 However, any type of substrate known in the art may be used in the methods of the present invention.

The delivery of a known amount of a selected *Bacillus* GST to a specific position on the support surface is preferably performed with a dispensing device equipped with one or more tips for insuring reproducible deposition and location of the GSTs and for 15 preparing multiple arrays. Any dispensing device known in the art may be used in the methods of the present invention. See, for example, U.S. Patent No. 5,807,522.

For liquid-dispensing on a hydrophilic surface, the liquid will have less of a tendency to bead, and the dispensed volume will be more sensitive to the total dwell time of the dispenser tip in the immediate vicinity of the support surface.

20 For liquid-dispensing on a hydrophobic surface, flow of fluid from the tip onto the support surface will continue from the dispenser onto the support surface until it forms a liquid bead. At a given bead size, *i.e.*, volume, the tendency of liquid to flow onto the surface will be balanced by the hydrophobic surface interaction of the bead with the support surface, which acts to limit the total bead area on the surface, and by the 25 surface tension of the droplet, which tends toward a given bead curvature. At this point, a given bead volume will have formed, and continued contact of the dispenser tip with the bead, as the dispenser tip is being withdrawn, will have little or no effect on bead volume.

The desired deposition volume, *i.e.*, bead volume, formed is preferably in the 30 range 2 pl (picoliters) to 2 nl (nanoliters), although volumes as high as 100 nl or more may be dispensed. It will be appreciated that the selected dispensed volume will depend on (i) the "footprint" of the dispenser tip(s), *i.e.*, the size of the area spanned by the tip(s),

(ii) the hydrophobicity of the support surface, and (iii) the time of contact with and rate of withdrawal of the tip(s) from the support surface. In addition, bead size may be reduced by increasing the viscosity of the medium, effectively reducing the flow time of liquid from the dispensing device onto the support surface. The drop size may be further 5 constrained by depositing the drop in a hydrophilic region surrounded by a hydrophobic grid pattern on the support surface.

At a given tip size, bead volume can be reduced in a controlled fashion by increasing surface hydrophobicity, reducing time of contact of the tip with the surface, increasing rate of movement of the tip away from the surface, and/or increasing the 10 viscosity of the medium. Once these parameters are fixed, a selected deposition volume in the desired picoliter to nanoliter range can be achieved in a repeatable fashion.

After depositing a liquid droplet of a *Bacillus* GST sample at one selected location on a support, the tip may be moved to a corresponding position on a second support, the GST sample is deposited at that position, and this process is repeated until 15 the GST sample has been deposited at a selected position on a plurality of supports.

This deposition process may then be repeated with another GST sample at another microarray position on each of the supports.

The diameter of each *Bacillus* GST region is preferably between about 20-200 μm . The spacing between each region and its closest (non-diagonal) neighbor, measured 20 from center-to-center, is preferably in the range of about 20-400 μm . Thus, for example, an array having a center-to-center spacing of about 250 μm contains about 40 regions/cm or 1,600 regions/cm². After formation of the array, the support is treated to evaporate the liquid of the droplet forming each region, to leave a desired array of dried, relatively flat GST regions. This drying may be done by heating or under vacuum. The DNA can also 25 be UV-crosslinked to the polymer coating.

Bacterial Cells

In the methods of the present invention, the two or more *Bacillus* cells may be any *Bacillus* cell where one of the cells is used as a reference for identifying differences in 30 expression of the same or similar complement of genes in the other cell(s). In one aspect, the two or more cells are the same cell. For example, they may be compared under different growth conditions, e.g., oxygen limitation, nutrition, and/or physiology. In

another aspect, one or more cells are mutants of the reference cell. For example, the mutant(s) may have a different phenotype. In a further aspect, the two or more cells are of different species (e.g., *Bacillus clausii* and *Bacillus subtilis*). In another further aspect, the two or more cells are of different genera. In an even further aspect, one or more cells
5 are transformants of the reference cell, wherein the one or more transformants exhibit a different property. For example, the transformants may have an improved phenotype relative to the reference cell and/or one of the other transformants. The term "phenotype" is defined herein as an observable or outward characteristic of a cell determined by its genotype and modulated by its environment. Such improved phenotypes may include,
10 but are not limited to, improved secretion or production of a protein or compound, reduced or no secretion or production of a protein or compound, improved or reduced expression of a gene, desirable morphology, an altered growth rate under desired conditions, relief of over-expression mediated growth inhibition, or tolerance to low oxygen conditions.
15 The *Bacillus* cells may be any *Bacillus* cells, but preferably *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus laetus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, or *Bacillus thuringiensis* cells.
20 In a preferred embodiment, the *Bacillus* cells are *Bacillus alkalophilus* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus amyloliquefaciens* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus brevis* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus circulans* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus clausii* cells. In another preferred
25 embodiment, the *Bacillus* cells are *Bacillus coagulans* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus firmus* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus laetus* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus lentus* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus licheniformis* cells. In another preferred
30 embodiment, the *Bacillus* cells are *Bacillus megaterium* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus pumilus* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus stearothermophilus* cells. In another

preferred embodiment, the *Bacillus* cells are *Bacillus subtilis* cells. In another preferred embodiment, the *Bacillus* cells are *Bacillus thuringiensis* cells.

In a more preferred embodiment, the *Bacillus* cells are *Bacillus licheniformis* cells. In a most preferred embodiment, the *Bacillus licheniformis* cells are *Bacillus licheniformis* ATCC 14580 cells.

In another more preferred embodiment, the *Bacillus* cells are *Bacillus clausii* cells. In another most preferred embodiment, the *Bacillus clausii* cells are *Bacillus clausii* NCIB 10309 cells.

In the methods of the present invention, the cells are cultivated in a nutrient medium suitable for growth using methods well known in the art for isolation of the nucleic acids to be used as probes. For example, the cells may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection).

20 Nucleic Acid Probes

The nucleic acid probes from the two or more *Bacillus* cells may be any nucleic acid including genomic DNA, cDNA, and RNA, and may be isolated using standard methods known in the art. For example, cDNA probes may be obtained from total RNA isolated from the cells using standard methods and reverse transcribed into total cDNA.

25 The populations of isolated nucleic acid probes may be labeled with colorimetric, radioactive (for example, ^{32}P , ^{33}P , or ^{35}S), fluorescent reporters, or other reporters using methods known in the art (Chen *et al.*, 1998, *Genomics* 51: 313-324; DeRisi *et al.*, 1997, *Science* 278: 680-686; U.S. Patent No. 5,770,367).

In a preferred embodiment, the probes are labeled with fluorescent reporters. For 30 example, the cDNA probes may be labeled during reverse transcription from the respective RNA pools by incorporation of fluorophores as dye-labeled nucleotides (DeRisi *et al.*, 1997, *supra*), e.g., Cy5-labeled deoxyuridine triphosphate, or the isolated

cDNAs may be directly labeled with different fluorescent functional groups. Fluorescent-labeled nucleotides include, but are not limited to, fluorescein conjugated nucleotide analogs (green fluorescence), lissamine nucleotide analogs (red fluorescence). Fluorescent functional groups include, but are not limited to, Cy3 (a green fluorescent dye) and Cy5 (red fluorescent dye).

Array Hybridization

The labeled nucleic acids from the two or more *Bacillus* cells are then added to a substrate containing an array of *Bacillus* GSTs under conditions where the nucleic acid pools from the two or more *Bacillus* cells hybridize to complementary sequences of the GSTs in the array. For purposes of the present invention, hybridization indicates that the labeled nucleic acids from the two or more cells hybridize to the GSTs under very low to very high stringency conditions.

A small volume of the labeled nucleic acids mixture is loaded onto the substrate. The solution will spread to cover the entire microarray. In the case of a multi-cell substrate, one or more solutions are loaded into each cell which stop at the barrier elements.

For nucleic acid probes of at least about 100 nucleotides in length, miroarray hybridization conditions described by Eisen and Brown , 1999, *Methods of Enzymology* 303: 179-205, may be used. Hybridization is conducted under a coverslip at 65°C in 3X SSC for 4-16 hours followed by post-hybridization at room temperature after removal of the coverslip in 2X SSC, 0.1% SDS by plunging the array two or three times in the solution, followed by successive washes in 1X SSC for 2 minutes and 0.2X SSC wash for to or more minutes.

Conventional conditions of very low to very high stringency conditions may also be used. Very low to very high stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 µg/ml sheared and denatured salmon sperm DNA, and either 25% formamide for very low and low stringencies, 35% formamide for medium and medium-high stringencies, or 50% formamide for high and very high stringencies, following standard Southern blotting procedures.

The carrier material is finally washed three times each for 15 minutes using 2 x SSC, 0.2% SDS preferably at least at 45°C (very low stringency), more preferably at least

at 50°C (low stringency), more preferably at least at 55°C (medium stringency), more preferably at least at 60°C (medium-high stringency), even more preferably at least at 65°C (high stringency), and most preferably at least at 70°C (very high stringency).

For shorter nucleic acid probes which are less than 50 nucleotides, microarray 5 hybridization conditions described by Kane *et al.*, 2000, *Nucleic Acids Research* 28: 4552-4557, may be used. Hybridization is conducted under a supported coverslip at 42°C for 16-18 hours at high humidity in 50% formamide, 4.1X Denhardt's, 4.4X SSC, and 100 µg/ml of herring sperm DNA. Arrays are washed after removal of the coverslip in 4X SSC by immersion into 1X SSC, 0.1% SDS for 10 minutes, 0.1X SSC, 0.1% SDS 10 twice for 10 minutes, and 0.1X SSC twice for 10 minutes.

For shorter nucleic acid probes which are about 50 nucleotides to about 100 nucleotides in length, conventional stringency conditions may be used. Such stringency conditions are defined as prehybridization, hybridization, and washing post-hybridization at 5°C to 10°C below the calculated T_m using the calculation according to Bolton and 15 McCarthy (1962, *Proceedings of the National Academy of Sciences USA* 48:1390) in 0.9 M NaCl, 0.09 M Tris-HCl pH 7.6, 6 mM EDTA, 0.5% NP-40, 1X Denhardt's solution, 1 mM sodium pyrophosphate, 1 mM sodium monobasic phosphate, 0.1 mM ATP, and 0.2 mg of yeast RNA per ml following standard Southern blotting procedures.

The carrier material is finally washed once in 6X SSC plus 0.1% SDS for 15 20 minutes and twice each for 15 minutes using 6X SSC at 5°C to 10°C below the calculated T_m .

The choice of hybridization conditions will depend on the degree of homology between the *Bacillus* GSTs and the nucleic acids obtained from the two or more *Bacillus* cells. For example, where the nucleic acid probes and the GSTs are obtained from 25 identical *Bacillus* cells, high stringency conditions may be most suitable. Where the cells are from a genus or species different from which the GSTs were obtained, low or medium stringency conditions may be more suitable.

In a preferred embodiment, the hybridization is conducted under low stringency conditions. In a more preferred embodiment, the hybridization is conducted under 30 medium stringency conditions. In a most preferred embodiment, the hybridization is conducted under high stringency conditions.

The entire solid support is then reacted with detection reagents if needed and

analyzed using standard calorimetric, radioactive, or fluorescent detection means. All processing and detection steps are performed simultaneously to all of the microarrays on the solid support ensuring uniform assay conditions for all of the microarrays on the solid support.

5

Detection

Any detection method known in the art may be used. The most common detection method is laser-induced fluorescence detection using confocal optics (Cheung *et al.*, 1998, *Nat. Genet.* 18: 225-230). The array is examined under fluorescence excitation conditions such that (i) the *Bacillus* GSTs in the array that hybridize to the nucleic acid probes obtained from one of the first cell and one or more second cells produces a distinct first fluorescence emission color or one or second fluorescence emission colors, respectively, and (ii) the *Bacillus* GSTs in the array that hybridize to substantially equal numbers of nucleic acid probes obtained from the first cell and one of the one or more second cells produce a distinct combined fluorescence emission color, respectively; wherein the relative expression of the genes in the two or more cells can be determined by the observed fluorescence emission color of each spot in the array.

The fluorescence excitation conditions are based on the selection of the fluorescence reporters. For example, Cy3 and Cy5 reporters are detected with solid state lasers operating at 532 nm and 632 nm, respectively.

Other methods of detection may be used employing colorimetric and radioactive (for example, ^{32}P , ^{33}P , or ^{35}S) reporters, or other reporters using methods known in the art (Chen *et al.*, 1998, *supra*; DeRisi *et al.*, 1997, *supra*; U.S. Patent No. 5,770,367).

25 **Data Analysis**

The fluorescence data obtained from the scanned image may then be analyzed using any of the commercially available image analysis software. The software preferably identifies array elements, subtracts backgrounds, deconvolutes multi-color images, flags or removes artifacts, verifies that controls have performed properly, and 30 normalizes the signals (Chen *et al.*, 1997, *Journal of Biomedical Optics* 2: 364-374).

Several computational methods have been described for the analysis and interpretation of microarray-based expression profiles including cluster analysis (Eisen *et*

al., 1998, *Proc. Nat. Acad. Sci. USA* 95: 14863-14868), parametric ordering of genes (Spellman *et al.*, 1998, *Mol. Biol. Cell* 9: 3273-3297), and supervised clustering methods based on representative hand-picked or computer-generated expression profiles (Chu *et al.*, 1998. *Science* 282: 699-705).

5

Computer Readable Media

The *Bacillus* GSTs described herein may be "provided" in a variety of media to facilitate their use. The term "provided" refers to a manufacture comprising an array of *Bacillus* GSTs. Such manufactures provide a large portion of the genome of *Bacillus* and parts thereof (e.g., an open reading frame (ORF)) in a form which allows one skilled in the art to examine the manufacture using means not directly applicable to examining the genome or a subset thereof as it exists in nature or in purified form.

Thus, the present invention also relates to such a manufacture in the form of a computer readable medium comprising an array of *Bacillus* GSTs selected from the group consisting of SEQ ID NOs. 1-8481, nucleic acid fragments of SEQ ID NOs. 1-8481, and nucleic acid sequences having preferably at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 1-8481.

In a preferred embodiment, the computer readable medium comprises an array of *Bacillus licheniformis* GSTs consisting of nucleic acid sequences of SEQ ID NOs. 1-4448.

In another preferred embodiment, the computer readable medium comprises an array of *Bacillus licheniformis* GSTs consisting of nucleic acid fragments of SEQ ID NOs. 1-4448.

In another preferred embodiment, the computer readable medium comprises an array of *Bacillus licheniformis* GSTs consisting of nucleic acid sequences having preferably at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 1-4448.

In another preferred embodiment, the computer readable medium comprises an array of *Bacillus clausii* GSTs consisting of nucleic acid sequences of SEQ ID NOs. 4449-8481.

In another preferred embodiment, the computer readable medium comprises an array of *Bacillus clausii* GSTs consisting of nucleic acid fragments of SEQ ID NOs. 4449-8481.

5 In another preferred embodiment, the computer readable medium comprises an array of *Bacillus clausii* GSTs consisting of nucleic acid sequences having preferably at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 4449-8481.

In one application of this embodiment, the *Bacillus* GSTs of the present invention can be recorded on computer readable media. The term "computer readable media" is 10 defined herein as any medium which can be read and accessed by a computer. Such computer readable media include, but are not limited to, magnetic storage media, e.g., floppy discs, hard disc storage medium, and magnetic tape; optical storage media, e.g., CD-ROM, DVD; electrical storage media, e.g., RAM and ROM; and hybrids of these categories, e.g., magnetic/optical storage media. One skilled in the art can readily 15 appreciate how any of the presently known computer readable media can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the 20 present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. One skilled in the art can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

25 A variety of data storage structures are available for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on 30 computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database

application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (e.g., text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

5 Various computer software are publicly available that allow a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form an array of *Bacillus clausii* GSTs selected from the group consisting of SEQ ID NOs. 4449-8481, nucleic acid fragments of SEQ ID NOs. 4449-8481, and nucleic acid sequences having preferably at least 85%, more preferably at 10 least 90%, and most preferably at least 95% homology to SEQ ID NOs. 4449-8481 enables one skilled in the art to routinely access the provided sequence information for a wide variety of purposes.

15 Software utilizing the BLAST (Altschul *et al.*, 1990, *Journal of Molecular Biology* 215: 403-410), BLAZE (Brutlag *et al.*, 1993, *Comp. Chem.* 17: 203-207), GENEMARK (Lukashin and Borodovsky, 1998, *Nucleic Acids Research* 26: 1107-1115), GENSCAN (Burge and Karlin, 1997, *Journal of Molecular Biology* 268: 78-94), GLIMMER (Salzberg *et al.*, 1998, *Nucleic Acids Research* 26: 544-548), and GRAIL (Xu *et al.*, 1994, *Comput. Appl. Biosci.* 10: 613-623) search algorithms may be used to identify open reading frames (ORFs) within a genome of interest, which contain 20 homology to ORFs or proteins from both *Bacillus licheniformis* and *Bacillus clausii* and from other organisms. Among the ORFs discussed herein are protein encoding fragments of the *Bacillus licheniformis* and *Bacillus clausii* genomes useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

25 The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, genes and gene products - many of which could be products themselves or used to genetically modify an industrial expression host through increased or decreased expression of a specific gene sequence(s).

30 The term "a computer-based system" is herein defined as the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-

based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. One skilled in the art can readily appreciate that any currently available computer-based system is suitable for use in the present invention.

5 As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

10 The term "data storage means" is defined herein as memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

15 The term "search means" refers is defined herein as one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means.

20 Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention.

25 Examples of such software includes, but is not limited to, MacPattern (Fuchs, 1991, *Comput. Appl. Biosci.* 7: 105-106), BLASTN and BLASTX National Center for Biotechnology Information (NCBI). One skilled in the art can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

30 The term "target sequence" is defined here as any DNA (genomic DNA, cDNA) or amino acid sequence of six or more nucleotides or two or more amino acids. One skilled in the art can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

The term "a target structural motif" or "target motif" is defined herein as any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target 5 motifs include, but are not limited to, enzyme active sites and signal sequences, substrate and cofactor binding domains, transmembrane domains, and sites for post-translational modifications. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences), repeats, palindromes, dyad symmetries, and transcription and translation start 10 and stop sites.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Bacillus licheniformis* or *Bacillus clausii* genomic sequences possessing varying degrees of homology to the target 15 sequence or target motif. Such presentation provides one skilled in the art with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Bacillus licheniformis* and *Bacillus clausii* genomes. For example, implementing software which 20 utilize the BLAST and BLAZE algorithms, described in Altschul *et al.*, 1990, *Journal of Molecular Biology* 215: 403-410, may be used to identify open reading frames within the *Bacillus licheniformis* or *Bacillus clausii* genome or the genomes of other organisms. A skilled artisan can readily recognize that any one of the publicly available homology 25 search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Substrates

30 The present invention also relates to substrates as described herein comprising an array of *Bacillus* GSTs.

In a preferred embodiment, the substrate comprises an array of *Bacillus licheniformis* GSTs selected from the group consisting of SEQ ID NOs. 1-4448, nucleic acid fragments of SEQ ID NOs. 1-4448, and nucleic acid sequences having preferably at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 1-4448. In a more preferred embodiment, the substrate comprises an array of *Bacillus licheniformis* GSTs selected from the group consisting of SEQ ID NOs. 1-4448. In another more preferred embodiment, the substrate comprises an array of *Bacillus licheniformis* GSTs selected from the group consisting of nucleic acid fragments of SEQ ID NOs. 1-4448. In another more preferred embodiment, the substrate comprises an array of *Bacillus licheniformis* GSTs selected from the group consisting of nucleic acid sequences having preferably at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 1-4448.

In a preferred embodiment, the substrate comprises an array of *Bacillus clausii* GSTs selected from the group consisting of SEQ ID NOs. 4449-8481, nucleic acid fragments of SEQ ID NOs. 4449-8481, and nucleic acid sequences having preferably at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 4449-8481. In a more preferred embodiment, the substrate comprises an array of *Bacillus clausii* GSTs selected from the group consisting of SEQ ID NOs. 4449-8481. In another more preferred embodiment, the substrate comprises an array of *Bacillus clausii* GSTs selected from the group consisting of nucleic acid fragments of SEQ ID NOs. 4449-8481. In another more preferred embodiment, the substrate comprises an array of *Bacillus clausii* GSTs selected from the group consisting of nucleic acid sequences having preferably at least 85%, more preferably at least 90%, and most preferably at least 95% homology to SEQ ID NOs. 4449-8481.

25

Co-linearity of *Bacillus licheniformis* and *Bacillus subtilis* chromosomes

The complete nucleotide sequence of the *Bacillus subtilis* chromosome was recently published (Kunst *et al.*, 1997, *Nature* 390: 249-256) and reveals the exact position of more than 4000 genes in this genome. Several public databases are available for searching and graphic representations of the entire genome (<http://genolist.pasteur.fr/SubtiList/>, http://locus.jouy.inra.fr/cgi-bin/genmic/madbase_home.pl, <http://bacillus.genome.ad.jp/>).

The method of shot-gun sequencing of the *Bacillus licheniformis* chromosome which is conducted herein does not directly address the specific arrangement of genes on the chromosome. However, since *Bacillus subtilis* and *Bacillus licheniformis* are very closely related organisms according to the literature (Ash *et al.*, 1991, *Letters in Applied Microbiology* 13: 202-206) the linear arrangement of genes on the two chromosomes might be similar.

To investigate this hypothesis, a series of long range PCR amplifications were made using primers to *Bacillus licheniformis* sequences which were identified as homologues to specific genes in *Bacillus subtilis*. Each PCR reaction employs *Bacillus licheniformis* chromosomal DNA as template for primer pairs that hybridizes to two genes in *Bacillus licheniformis* which has a known location, orientation and distance in the *Bacillus subtilis* homologs. If a PCR product of the expected size is synthesized, according to the *Bacillus subtilis* chromosomal map, it can be concluded that the two target genes are placed in the same orientation and at the same distance on both chromosomes.

Multiple PCR reactions as described herein were performed on *Bacillus licheniformis* to investigate the degree of co-linearity to the model organism *Bacillus subtilis*. The results of the PCR mapping indicate that approximately 75% of the *Bacillus subtilis* and *Bacillus licheniformis* gene content are similar or collinear (Lapidus *et al.*, 20 Poster P67 at The 10th International Conference on Bacilli, Baveno, Italy).

This high degree of co-linearity between these two organisms can be exploited when yet unidentified genes or part of genes from the *Bacillus licheniformis* chromosome are to be cloned. By using the *Bacillus subtilis* chromosomal map as model for the *Bacillus licheniformis* chromosome, it is possible to amplify specific genome regions of *Bacillus licheniformis* where a certain gene of interest are predicted to be located according to the *Bacillus subtilis* chromosomal map. Flanking sequence tags to the region can be as far apart as 10-15 kb when long range PCR methods are employed. This method of PCR mapping was used for cloning several genes of specific interest that were not tagged in the primary shot-gun library.

30

Gene disrupting/deletion

Figure 1 describes a method to make deletions at specific loci of the *Bacillus licheniformis* or *Bacillus clausii* chromosome utilizing the *Bacillus licheniformis* or *Bacillus clausii* GST sequences, respectively, described herein.

A plasmid denoted "Deletion plasmid" is constructed by cloning two PCR 5 amplified fragments from given gene X region denoted "Y" on a temperature-sensitive parent plasmid. The PCR fragments are denoted "A" and "B", wherein A comprises the 5'- part of the Y fragment; and B comprises the 3'-part of DNA fragment Y. The deleted Y DNA between A and B may be varied depending of the size of the Y fragment. The size of the A and B fragment should be larger than 100 basepairs. A spectinomycin 10 resistance gene flanked by resolvase (*res*) sites is introduced between fragments "A" and "B" on the plasmid. This spectinomycin resistance gene can later be removed by resolvase-mediated site-specific recombination.

The disrupting/deletion is transferred from the "Deletion plasmid" to the 15 chromosome of a *Bacillus licheniformis* or *Bacillus clausii* target strain by double homologous recombination via fragments "A" and "B", mediated by integration and excision of the temperature-sensitive plasmid. The resulting strain is denoted "Deletion strain".

The present invention is further described by the following examples, which 20 should not be construed as limiting the scope of the invention.

Examples

Chemicals used as buffers and substrates were commercial products of at least 25 reagent grade.

Example 1: Construction of *Bacillus licheniformis* library

Bacillus licheniformis ATCC 14580 was used as source of chromosomal DNA for constructing a library. Strain *E. coli* JJC 128F' *araD139* Δ (*ara-leu*)7696 *galE15* *galK16* 30 Δ (*lac*)*X74* *hsdr*⁻ *hsdm*⁺ *Str*^R F'[*lacI*^q Δ (*lacZ*)*M15* *traD36*] was used as a host to construct the genomic bank (Sorokin *et al.*, 1996, *Microbiology* 142: 2005-2016).

Chromosomal DNA from *Bacillus licheniformis* ATCC 14580 was prepared as follows. *Bacillus licheniformis* strain ATCC 14580 was cultivated overnight at 37°C in 125 ml shake flasks containing 25 ml of LB medium (Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, NY, 1989). The cells were harvested and treated with 10 µg of lysozyme per ml of 50 mM Tris-HCl pH 8.0, 50 mM EDTA, 25% sucrose. SDS was then added to a final concentration of 0.5% followed by proteinase K to 100 µg/ml. The mixture was incubated at 50°C for 4 hours, and then extracted three times with water-saturated phenol-chloroform (1:1 v/v) at pH 8.0. After precipitation with two volumes of ethanol in 0.3 M sodium acetate pH 4.8, the DNA was removed with a glass rod, washed in 70% ethanol, and stored at -20°C in water at 100 µg/ml.

Plasmid pSGMU2 (Errington, 1986, *Journal of General Microbiology* 132: 2953-2961) was used as a vector for constructing the chromosomal bank. pSGMU2 was isolated as follows. Cells of *E. coli* JJC 128F', containing pSGMU2, were grown in 4 ml of 2X YT medium (Sambrook *et al.*, 1989, *supra*) overnight. The cell pellet was resuspended in 100 µl of 50 mM glucose, 25 mM Tris/HCl pH 8.0, 10 mM EDTA solution (TE). Then a 100 µl volume of 10 mg/ml lysozyme was added. After 30 minutes 400 µl of 1% (w/v) SDS, 0.2 M NaOH were added. After cell lysis, 300 µl of 3 M sodium acetate pH 4.8, was added. After 30 minutes on ice, tubes were centrifuged at 13,000 rpm (5000 x g) for 1 hour and 0.6 ml of isopropanol was added to the supernatant. After centrifugation as before for 10 minutes, the pellet was dissolved in 100 µl of water and then 100 µl of 9 M lithium chloride was added. After 1 hour at -20°C, tubes were centrifuged at 13,000 rpm (5000 x g) for 10 minutes. The pellet was discarded and 500 µl of absolute ethanol was added to the supernatant. The pellet was redissolved in 300 µl of 0.3 M sodium acetate pH 4.8 and precipitated again. After dissolving the pellet in 100 µl of TE, the plasmid preparation was sufficiently pure for fluorescent sequencing.

A library with insert sizes in the range from 1 to 2 kb, was constructed by using pSGMU2. A 20 µg quantity of *Bacillus licheniformis* chromosomal DNA was sonicated using a VibraCell 72408 sonicator (Bioblock Scientific) at minimal amplitude for 10 seconds. The sonication was performed in 300 µl of Bal31 buffer (600 mM NaCl, 20 mM Tris-HCl pH 8.0, 12 mM CaCl₂, 12 mM MgCl₂, 1 mM EDTA) in a 1.5 ml Eppendorf tube. After sonication the chromosomal DNA was treated with Bal31

exonuclease (New England Biolabs, Inc., Beverly, MA) for 5 minutes at 25°C. After water-saturated phenol extraction and ethanol precipitation the DNA was treated by Klenow fragment of DNA polymerase I under the following conditions: 10 mM Tris HCl pH 7.6, 10 mM MgCl₂, 0.2 mM each dNTP, at 37°C for 1 hour. After water-saturated phenol extraction and ethanol precipitation, the DNA was ligated with *Sma*I-digested pSGMU2 and treated with bacterial alkaline phosphatase. The ligation was performed in 10 mM Tris HCl pH 7.6, 10 mM MgCl₂, 1 mM DTT, 1 mM ATP at 10°C for 6 hours. DNA from the ligation mixture was precipitated with ethanol in the presence of 1 mM glycogen at -20°C.

10 The DNA was then electroporated into *E. coli* JJC128F' cells using 2.5kV and 25 mF. The cells were plated on LB agar medium containing 50 µg/ml of ampicillin for selection of transformants and 20 µg/ml of 5-bromo-4-chloro-3-indolyl beta-D-galactopyranoside (XGAL) and 20 µg/ml of isopropyl beta-D-thiogalactopyranoside (IPTG) for selection of inserts. The ratio of white to blue colonies in a successful 15 experiment was 4 to 1. A total of 25.244 plasmids were extracted from the white colonies and were sequenced by forward (M13-21) primer and 877 plasmids by reverse (M13RP1) primer using a Perkin-Elmer Applied Biosystems Model 377 XL Automatic DNA Sequencer, Perkin-Elmer Applied Biosystems, Inc., Foster City, CA) with successful sequencing rate of about 90%. The sequencing produced a total of 13.227.856 20 bases. The total accumulated nonredundant contig length was 3.723.871 basepairs in 1.239 contigs randomly distributed over the chromosome.

Oligonucleotides were synthesized using a DNA Synthesizer "Oligo 1000" (Beckman-Coulter, Fullerton, CA). Primers used for Long Accurate PCR were 20-22-mers, chosen to contain 12 GC-bases.

25 Plasmid DNA for sequencing was prepared as described above. PCR products used for sequencing with dye terminators were purified by the Wizard™ PCR Preps kit (Promega, Madison, WI) or agarose gel electrophoresis. Forward and reverse PCR sequencing was performed using BigDye terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer Applied Biosystems, Inc., Foster City, CA) and a "Perkin Elmer" 9600 30 thermal cycler or the "Catalyst" station (Perkin-Elmer Applied Biosystems, Inc., Foster City, CA). The fragment separation was conducted using an Applied Biosystems Model 377 XL Automatic DNA Sequencer.

The Long Accurate PCR reaction (50 μ l) contained the following components as described by Sorokin *et al.* (1996, *Genome Research* 6: 448-453): 20 mM Tricine, pH 8.7; 85 mM potassium acetate; 1 mM magnesium acetate; 8% glycerol; 2% dimethylsulfoxide; 0.2 mM each dNTP; 0.2 μ M each primer; 0.1 μ g chromosomal DNA; 5 2 U rTth (Perkin-Elmer Applied Biosystems, Inc., Foster City, CA); and 0.05 U of Vent polymerase (New England Biolabs, Inc., Beverly, MA). The Long Accurate PCR used the following cycling conditions: One cycle at 94°C for 5 minutes; 12 cycles of 10 second melting at 94°C, and 12 minutes annealing-polymerisation-repair at 68°C; and 24 cycles with increasing the extension time 15 seconds for each cycle.

10 The overall results are summarized in Table 1.

Table 1. Summary of whole-genome random clone sequencing of *Bacillus licheniformis* ATCC 14580

| | | |
|----|---------------------------------|-----------|
| 15 | Successful sequencing reactions | 22,468 |
| | Total contig length (bp) | 3,723,871 |
| | Number of contigs | 1,239 |
| | Average contig length (bp) | 3,006 |

20 **Example 2: DNA Sequencing and Analysis of Nucleotide Sequence Data of the *Bacillus licheniformis* GST Libraries**

Nucleotide sequence data were scrutinized for quality, and samples giving improper spacing or ambiguity levels exceeding 2% were discarded or re-run. Vector sequences were removed with the crossmatch program from the Phred/Phrap package 25 (Ewing and Green, 1998, *Genome Research* 8: 186-194). The sequences were assembled with Phrap also from the Phred/Phrap package.

Annotation of a gene means assignment of a function to a given sequence. The protein encoded genes were found and annotated the following way: The assembled sequences were searched with BLASTX (Pearson and Lipman, 1988, *Proceedings of the 30 National Academy of Science USA* 85: 2444-2448; Pearson, 1990, *Methods in Enzymology* 183: 63-98) against a customized database consisting of protein sequences from SWISSPROT, SWISSPROTNEW, TREMBL, TREMBLNEW, REMTREMBL, PDB and GeneSeqP. The matrix used was BL50. The start and stop position of each hit and the score of the hit were temporarily marked in the sequence. All open reading

frames starting with ATG, GTG or TTG were temporarily marked with the start and stop position and a score. The score of the ORF was calculated as 0.5 times the length of the ORF for ORF starting with ATG and 0.25 times the length of the ORF for ORFs starting with GTG or TTG. A non overlapping set of regions with maximal score larger than 100 was found from the temporarily marked sequence. Each region represents a gene. The best hit for each gene is shown in Appendix 1. Functional category assignment was done by fastx homology search against clusters of orthologous genes from ncbi (<http://www.ncbi.nlm.nih.gov/COG/>). In Appendix 1, the assignment to a particular functional category is represented by a single letter. "C" means energy production and conversion. "D" means cell division and chromosome partitioning. "E" means amino acid transport and metabolism. "F" means nucleotide transport and metabolism. "G" means carbohydrate transport and metabolism. "H" means coenzyme metabolism. "I" means lipid metabolism. "J" means translation, ribosomal structure and biogenesis. "K" means transcription. "L" means DNA replication, recombination and repair. "M" means cell envelope biogenesis, outer membrane. "N" means cell motility and secretion. "O" means posttranslational modification, protein turnover, chaperones. "P" means inorganic ion transport and metabolism. "Q" means secondary metabolites biosynthesis, transport and catabolism. "R" means general function prediction only. "S" means function unknown. "T" means signal transduction mechanisms.

20 Structural RNA encoding genes were found by homology (blastn) to tRNA and rRNA genes in *Bacillus subtilis*. The *Bacillus subtilis* data were extracted from <http://genolist.pasteur.fr/SubtiList/>.

The *Bacillus licheniformis* GST sequences are designated SEQ ID NOs. 1-4448. An "N" in a nucleic acid sequence means that the nucleotide is an A, C, G, or T.

25

Example 3: Construction of *Bacillus clausii* library

Bacillus clausii NCIB 10309 (National Collections of Industrial and Marine Bacteria Ltd., 23 St. Machar Drive, Aberdeen, Scotland, UK AB2 1RY) was used as source of chromosomal DNA for constructing a library. Strain *E. coli* JJC 128F' 30 *araD139* Δ (*ara-leu*)7696 *galE15* *galK16* Δ (*lac*)X74 *hsdR*⁻ *hsdM*⁺ *Str*^R *F'*[*lacI*^Q Δ (*lacZ*)M15 *traD36*] was used as a host to construct the genomic bank (Sorokin *et al.*, 1996, *Microbiology* 142: 2005-2016).

Chromosomal DNA from *Bacillus clausii* NCIB 10309 was prepared as follows. *Bacillus clausii* strain NCIB 10309 was cultivated overnight at 37°C in 125 ml shake flasks containing 25 ml of LB medium (Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, NY, 1989). The cells 5 were harvested and treated with 10 µg of lysozyme per ml of 50 mM Tris-HCl pH 8.0, 50 mM EDTA, 25% sucrose. SDS was then added to a final concentration of 0.5% followed by proteinase K to 100 µg/ml. The mixture was incubated at 50°C for 4 hours, and then extracted three times with water-saturated phenol-chloroform (1:1 v/v) at pH 8.0. After precipitation with two volumes of ethanol in 0.3 M sodium acetate pH 4.8, the DNA was 10 removed with a glass rod, washed in 70% ethanol, and stored at -20°C in water at 100 µg/ml.

Plasmid pSGMU2 (Errington, 1986, *Journal of General Microbiology* 132: 2953-2961) was used as a vector for constructing the chromosomal bank. pSGMU2 was isolated as follows. Cells of *E. coli* JJC 128F', containing pSGMU2, were grown in 4 ml 15 of 2X YT medium (Sambrook *et al.*, 1989, *supra*) overnight. The cell pellet was resuspended in 100 µl of 50 mM glucose, 25 mM Tris/HCl pH 8.0, 10 mM EDTA solution (TE). Then a 100 µl volume of 10 mg/ml lysozyme was added. After 30 minutes 400 µl of 1% (w/v) SDS, 0.2 M NaOH were added. After cell lysis, 300 µl of 3 M sodium acetate pH 4.8, was added. After 30 minutes on ice, tubes were centrifuged at 20 13,000 rpm (5000 x g) for 1 hour and 0.6 ml of isopropanol was added to the supernatant. After centrifugation as before for 10 minutes, the pellet was dissolved in 100 µl of water and then 100 µl of 9 M lithium chloride was added. After 1 hour at -20°C, tubes were centrifuged at 13,000 rpm (5000 x g) for 10 minutes. The pellet was discarded and 500 µl of absolute ethanol was added to the supernatant. The pellet was redissolved in 300 µl 25 of 0.3 M sodium acetate pH 4.8 and precipitated again. After dissolving the pellet in 100 µl of TE, the plasmid preparation was sufficiently pure for fluorescent sequencing.

A library with insert sizes in the range from 1 to 2 kb, was constructed by using pSGMU2. A 20 µg quantity of *Bacillus clausii* chromosomal DNA was sonicated using a VibraCell 72408 sonicator (Bioblock Scientific) at minimal amplitude for 10 seconds. 30 The sonication was performed in 300 µl of Bal31 buffer (600 mM NaCl, 20 mM Tris-HCl pH 8.0, 12 mM CaCl₂, 12 mM MgCl₂, 1 mM EDTA) in a 1.5 ml Eppendorf tube. After sonication the chromosomal DNA was treated with Bal31 exonuclease (New

England Biolabs, Inc., Beverly, MA) for 5 minutes at 25°C. After water-saturated phenol extraction and ethanol precipitation the DNA was treated by Klenow fragment of DNA polymerase I under the following conditions: 10 mM Tris HCl pH 7.6, 10 mM MgCl₂, 0.2 mM each dNTP, at 37°C for 1 hour. After water-saturated phenol extraction and 5 ethanol precipitation, the DNA was ligated with *Sma*I-digested pSGMU2 and treated with bacterial alkaline phosphatase. The ligation was performed in 10 mM Tris HCl pH 7.6, 10 mM MgCl₂, 1 mM DTT, 1 mM ATP at 10°C for 6 hours. DNA from the ligation mixture was precipitated with ethanol in the presence of 1 mM glycogen at -20°C.

The DNA was then electroporated into *E. coli* JJC128F' cells using 2.5kV and 25 10 mF. The cells were plated on LB agar medium containing 50 µg/ml of ampicillin for selection of transformants and 20 µg/ml of 5-bromo-4-chloro-3-indolyl beta-D-galactopyranoside (XGAL) and 20 µg/ml of isopropyl beta-D-thiogalactopyranoside (IPTG) for selection of inserts. The ratio of white to blue colonies in a successful experiment was 4 to 1. A total of 6,554 plasmids were extracted from the white colonies 15 and were sequenced by forward (M13-21) primer using a Perkin-Elmer Applied Biosystems Model 377 XL Automatic DNA Sequencer, Perkin-Elmer Applied Biosystems, Inc., Foster City, CA) with successful sequencing rate of about 90%. The sequencing produced 3,191,401 bp. The total accumulated nonredundant contig length was 2,022,840 bp in 2,232 contigs randomly distributed over the chromosome.

20 Oligonucleotides were synthesized using a DNA Synthesizer "Oligo 1000" (Beckman-Coulter, Fullerton, CA). Primers used for Long Accurate PCR were 20-22-mers, chosen to contain 12 GC-bases.

The overall results are summarized in Table 2.

25 Table 2. Summary of whole-genome random clone sequencing of *Bacillus clausii*

| | | |
|----|---------------------------------------|-----------|
| | Successful sequencing reactions | 5,899 |
| | Total characters in gel readings (bp) | 3,191,401 |
| | Average gel read length (bp) | 541 |
| 30 | Total contig length (bp) | 2,022,840 |
| | Number of contigs | 2,232 |

Example 4: Analysis of Nucleotide Sequence Data of the *Bacillus clausii* GST Libraries

Nucleotide sequence data were scrutinized for quality, and samples giving improper spacing or ambiguity levels exceeding 2% were discarded or re-run. Vector sequences were removed with the crossmatch program from the Phred/Phrap package (Ewing and Green, 1998, *Genome Research* 8: 186-194). The sequences were assembled with Phrap also from the Phred/Phrap package.

Annotation of a gene means assignment of a function to a given sequence. The protein encoded genes were found and annotated the following way: The assembled sequences were searched with BLASTX (Pearson and Lipman, 1988, *Proceedings of the National Academy of Science USA* 85: 2444-2448; Pearson, 1990, *Methods in Enzymology* 183: 63-98) against a customized database consisting of protein sequences from SWISSPROT, SWISSPROTNEW, TREMBL, TREMBLNEW, REMTREMBL, PDB and GeneSeqP. The matrix used was BL50. The start and stop position of each hit and the score of the hit were temporarily marked in the sequence. All open reading frames starting with ATG, GTG or TTG were temporarily marked with the start and stop position and a score. The score of the ORF was calculated as 0.5 times the length of the ORF for ORF starting with ATG and 0.25 times the length of the ORF for ORFs starting with GTG or TTG. A non overlapping set of regions with maximal score larger than 100 was found from the temporarily marked sequence. Each region represents a gene. The best hit for each gene is shown in Appendix 2. Functional category assignment was done by fastx homology search against clusters of orthologous genes from ncbi (<http://www.ncbi.nlm.nih.gov/COG/>). In Appendix 2, the assignment to a particular functional category is represented by a single letter. "C" means energy production and conversion. "D" means cell division and chromosome partitioning. "E" means amino acid transport and metabolism. "F" means nucleotide transport and metabolism. "G" means carbohydrate transport and metabolism. "H" means coenzyme metabolism. "T" means lipid metabolism. "J" means translation, ribosomal structure and biogenesis. "K" means transcription. "L" means DNA replication, recombination and repair. "M" means cell envelope biogenesis, outer membrane. "N" means cell motility and secretion. "O" means posttranslational modification, protein turnover, chaperones. "P" means inorganic ion transport and metabolism. "Q" means secondary metabolites

biosynthesis, transport and catabolism. "R" means general function prediction only. "S" means function unknown. "T" means signal transduction mechanisms.

Structural RNA encoding genes were found by homology (blastn) to tRNA and rRNA genes in *Bacillus subtilis*. The *Bacillus subtilis* data were extracted from 5 <http://genolist.pasteur.fr/SubtiList/>.

The *Bacillus clausii* GST sequences, which encode proteins are designated SEQ ID NOs. 4449-8481. An "N" in a nucleic acid sequence means that the nucleotide is an A, C, G, or T.

10 **Example 5: DNA Microarrays**

Details of the construction of a typical microarrayer can be found on the world wide web site of Professor Patrick Brown of Stanford University at the following URL: <http://cmgm.stanford.edu/pbrown/mguide/index.html>. Scanners and computer software for analysis of DNA microarrays are available from several commercial sources such as 15 General Scanning Inc. (Watertown, MA; see http://www.genscan.com/sales/loc_lifesci.html), or Axon Instruments (Foster City, CA; see <http://www.axon.com>).

Individual *Bacillus* GST clones were purified as plasmid minipreps using Qiagen Biorobot 9600 (QIAGEN, Inc., Valencia, CA). The plasmid minipreps were precipitated 20 with isopropanol, aliquoted and stored as described on the web site of Professor Patrick Brown of Stanford University at the following URL: <http://cmgm.stanford.edu/pbrown/mguide/index.html>.

The amplified GST targets prepared in this manner were spotted individually onto polylysine-coated glass slides using a microarrayer device as described by DeRisi *et al.* 25 (1997, *Science* 278: 680-686). For additional details, see <http://cmgm.stanford.edu/pbrown/protocols/index.html>). The microarrays were probed with fluorescently labeled cDNA prepared by reverse transcription of polyadenylated mRNA (DeRisi *et al.*, 1997, *supra*) extracted from *Bacillus* cells (Example 2 or Example 4). Conditions for pretreatment of the microarrays, hybridization and washing conditions 30 have been described previously (DeRisi *et al.*, 1997, *supra*; see also <http://cmgm.stanford.edu/pbrown/protocols/index.html>).

To increase the reliability with which changes in expression levels could be

discerned, probes prepared from induced or treated cells were labeled with the red fluorescent dye, Cy5 (Amersham Corporation, Arlington Heights, IL), and mixed with probes from uninduced, untreated, or "reference" cells were labeled with a green fluorescent dye, Cy3 (Amersham Corporation, Arlington Heights, IL) using the procedure 5 described by <http://cmgm.stanford.edu/pbrown/protocols/index.html>. The relative ratio of fluorescence intensity measured for the Cy3 and Cy5 fluorophors corresponding to each GST target in the arrays was determined using ScanAlyze software, available free of charge at <http://rama.stanford.edu/software/>. This provides a reliable measure of the relative abundance of the corresponding mRNA in the two cell populations (e.g., treated 10 cells versus reference cells).

The invention described and claimed herein is not to be limited in scope by the specific embodiments herein disclosed, since these embodiments are intended as 15 illustrations of several aspects of the invention. Any equivalent embodiments are intended to be within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. In the case of conflict, the present disclosure including definitions will control.

20 Various references are cited herein, the disclosures of which are incorporated by reference in their entireties.

Appendix 1: *Bacillus licheniformis* annotation and divisions into functional categories

Information storage and processing

5

- J 1154-1309 Translation, ribosomal structure and biogenesis
- K 1310-1521 Transcription
- 10 L 1522-1665 DNA replication, recombination and repair

Cellular processes

15

- D 174-218 Cell division and chromosome partitioning
- O 1925-2015 Posttranslational modification, protein turnover, chaperones
- M 1666-1835 Cell envelope biogenesis, outer membrane
- 20 N 1836-1924 Cell motility and secretion
- P 2016-2165 Inorganic ion transport and metabolism

25

Metabolism

- C 1-173 Energy production and conversion
- 30 G 642-967 Carbohydrate transport and metabolism
- E 219-554 Amino acid transport and metabolism
- F 555-641 Nucleotide transport and metabolism
- 35 H 968-1073 Coenzyme metabolism
- I 1074-1153 Lipid metabolism
- 40 Q 2166-2287 Secondary metabolites biosynthesis, transport and catabolism

Structural RNA

45

- Z 4361-4448 tRNA and rRNA

Functional category not assigned

- R 2288-2621 Functional category not assigned

S 2622-4236 Functional category not assigned

| | | | |
|----|------------|---|----------------------------------------------------------------|
| 5 | ID0001 | C | NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4). |
| | ID0002 | C | PYRUVATE CARBOXYLASE (EC 6.4.1.1). |
| | ID0003 | C | QUINOL OXIDASE POLYPEPTIDE I (EC 1.9.3.-) (QUINOL OXIDASE AA) |
| 10 | ID0004 | C | NITRITE REDUCTASE [NAD(P)H] (EC 1.6.6.4). |
| | ID0005 | C | HYPOTHETICAL 79.2 KDA PROTEIN IN ACDA 5'REGION. |
| | ID0006 | C | FORMATE DEHYDROGENASE ALPHA CHAIN. |
| | ID0007 | C | 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2) (ALPH |
| | ID0008 | C | FORMATE ACETYLTRANSFERASE. |
| | ID0009 | C | PUTATIVE FORMATE DEHYDROGENASE. |
| 15 | ID0010 | C | 68% IDENTITY PROTEIN TO 1-PYRROLINE-5-CARBOXYLATE DEHYDROGEN |
| | ID0011 | C | L-RIBULOKINASE (EC 2.7.1.16). |
| | ID0012 | C | YVFW PROTEIN. |
| | ID0013 | C | ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) (VEGETATIVE |
| 20 | PROTEIN 31 | | CYTOCHROME CAA3 OXIDASE (SUBUNIT I). |
| | ID0014 | C | ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34) (VEGETATIVE |
| | ID0015 | C | PROTEIN 1 |
| | ID0016 | C | PTS SYSTEM, MANNITOL-SPECIFIC IIABC COMPONENT (EIIABC-MTL) (|
| 25 | ID0017 | C | L-LACTATE PERMEASE. |
| | ID0018 | C | FUMARATE HYDRATASE, CLASS-II (EC 4.2.1.2) (FUMARASE). |
| | ID0019 | C | AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5). |
| 30 | ID0020 | C | ALCOHOL-ACETALDEHYDE DEHYDROGENASE. |
| | ID0021 | C | CitM protein. |
| | ID0022 | C | ISOCITRATE DEHYDROGENASE. |
| | ID0023 | C | ASSIMILATORY NITRATE REDUCTASE CATALYTIC SUBUNIT (EC 1.7.99. |
| 35 | ID0024 | C | HOMOLOGUE OF SUCCINATE SEMIALDEHYDE DEHYDROGENASE GABD OF E. |
| | ID0025 | C | HYPOTHETICAL 50.9 KDA PROTEIN. |
| | ID0026 | C | PROTON GLUTAMATE SYMPORT PROTEIN (GLUTAMATE-ASPARTATE CARRIE |
| 40 | ID0027 | C | NADP-DEPENDENT ALDEHYDE DEHYDROGENASE (EC 1.2.1.3). |
| | ID0028 | C | PROBABLE NADH-DEPENDENT BUTANOL DEHYDROGENASE 1 (EC 1.1.1.-) |
| | ID0029 | C | NADH DEHYDROGENASE-LIKE PROTEIN. |
| | ID0030 | C | HYPOTHETICAL 47.8 KDA PROTEIN. |
| 45 | ID0031 | C | PROBABLE MALATE OXIDOREDUCTASE [NAD] (EC 1.1.1.38) (MALIC EN |
| | ID0032 | C | HYPOTHETICAL 54.6 KDA PROTEIN. |
| | ID0033 | C | HYPOTHETICAL NA+/H+ ANTIPORTER IN ANSB-SP01IM INTERGENIC REG |
| 50 | ID0034 | C | Staphylococcus aureus mutant P10B2 virulence gene product. |
| | ID0035 | C | CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-) |
| 55 | ID0036 | C | SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5) (SCS- ALPHA) (|
| | ID0037 | C | CITRATE SYNTHASE II (EC 4.1.3.7). |
| | ID0038 | C | DIHYDROLIPOAMIDE DEHYDROGENASE COMPONENT OF PYRUVATEDEHYDROG |
| | ID0039 | C | METHYLMALONATE-SEMALALDEHYDE DEHYDROGENASE. |
| 60 | ID0040 | C | HYPOTHETICAL 44.9 KDA PROTEIN. |
| | ID0041 | C | PROBABLE NAD-DEPENDENT MALIC ENZYME (EC 1.1.1.38) (NAD-ME). |

| | | | |
|----|---------------------|---|-------------------------------------------------------|
| | ID0042 | C | ASSIMILATORY NITRATE REDUCTASE ELECTRON TRANSFER |
| | SUBUNIT. | | |
| | ID0043 | C | PUTATIVE BUTYRATE KINASE (EC 2.7.2.7) (BK). |
| | ID0044 | C | HYPOTHETICAL 37.1 KDA PROTEIN IN ARA-LACA INTERGENIC |
| 5 | REGION. | | |
| | ID0045 | C | 2-OXOISOVALERATE DEHYDROGENASE ALPHA SUBUNIT (EC |
| | 1.2.4.4.) (B | | |
| | ID0046 | C | PYRUVATE DEHYDROGENASE E2 (DIHYDROLIPOAMIDE |
| | ACETYLTRANSFERAS | | |
| 10 | ID0047 | C | IOLS PROTEIN (VEGETATIVE PROTEIN 147) (VEG147). |
| | ID0048 | C | 2-OXOISOVALERATE DEHYDROGENASE BETA SUBUNIT (EC |
| | 1.2.4.4.) (BR | | |
| | ID0049 | C | GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL 3- |
| | PHOSPHOTRANSFE | | |
| 15 | ID0050 | C | CYTOCHROME C OXIDASE POLYPEPTIDE II PRECURSOR (EC |
| | 1.9.3.1.) (| | |
| | ID0051 | C | SUCCINYL-COA SYNTHETASE (ALPHA SUBUNIT). |
| | ID0052 | C | PROBABLE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE YQJM |
| | (EC 1.--- | | |
| 20 | ID0053 | C | HOMOLOGOUS TO CITRATE-SODIUM SYMPORT. |
| | ID0054 | C | YFMT. |
| | ID0055 | C | ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT (ALPHA- |
| | ETF) (EL | | |
| | ID0056 | C | MALATE DEHYDROGENASE (EC 1.1.1.37) (VEGETATIVE |
| 25 | PROTEIN 69) | (| |
| | ID0057 | C | SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC |
| | 1.3.99.1). | | |
| | ID0058 | C | Corynebacterium thermoaminogenes acn protein. |
| | ID0059 | C | PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT |
| 30 | (EC 1.2.4 | | |
| | ID0060 | C | PYRUVATE DEHYDROGENASE BETA SUBUNIT PDHB (EC |
| | 1.2.4.1). | | |
| | ID0061 | C | PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN (GLUTAMATE- |
| | ASPARTATE | | |
| 35 | ID0062 | C | GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD(P)+] (EC |
| | 1.1.1.94) (| | |
| | ID0063 | C | SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC |
| | 1.3.99.1). | | |
| | ID0064 | C | LIPOAMIDE ACYLTRANSFERASE COMPONENT OF BRANCHED-CHAIN |
| 40 | ALPHA- | | |
| | ID0065 | C | QUINOL OXIDASE POLYPEPTIDE II PRECURSOR (EC 1.9.3.-) |
| | (QUINOL | | |
| | ID0066 | C | PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8) |
| | (PHOSPHOTRANSACETYL | | |
| 45 | ID0067 | C | Bacillus subtilis ypgA clade protein. |
| | ID0068 | C | H(+)/SODIUM-GLUTAMATE SYMPORTER. |
| | ID0069 | C | ACETATE KINASE (EC 2.7.2.1) (ACETOKINASE). |
| | ID0070 | C | HYPOTHETICAL 49.2 KDA PROTEIN. |
| | ID0071 | C | PUTATIVE L-LACTATE PERMEASE YVFH. |
| 50 | ID0072 | C | PUTATIVE MALATE DEHYDROGENASE (EC 1.1.1.37). |
| | ID0073 | C | L-LACTATE DEHYDROGENASE (EC 1.1.1.27). |
| | ID0074 | C | CITRATE SYNTHASE I (EC 4.1.3.7). |
| | ID0075 | C | PUTATIVE MALOLACTIC ENZYME (EC 1.----) [INCLUDES: |
| | MALIC ENZ | | |
| 55 | ID0076 | C | FDHD PROTEIN HOMOLOG. |
| | ID0077 | C | HYPOTHETICAL 37.6 KDA PROTEIN. |
| | ID0078 | C | HYPOTHETICAL 35.0 KDA PROTEIN IN RAPJ-OPUAA |
| | INTERGENIC REGIO | | |
| | ID0079 | C | NITRATE REDUCTASE GAMMA CHAIN (EC 1.7.99.4). |
| 60 | ID0080 | C | HYPOTHETICAL 36.6 KDA PROTEIN IN QOXD-VPR INTERGENIC |
| | REGION. | | |
| | ID0081 | C | HYPOTHETICAL 49.0 KDA PROTEIN. |
| | ID0082 | C | MALATE SYNTHASE (EC 4.1.3.2). |
| | ID0083 | C | YTHA. |
| 65 | ID0084 | C | Glycerol dehydrogenase. |
| | ID0085 | C | FERRIC LEGHEMOGLOBIN REDUCTASE-2 PRECURSOR. |

| | | | |
|----|--------------|---|-------------------------------------------------------------------------|
| | ID0086 | C | OXIDOREDUCTASE, N5,N10-METHYLENETETRAHYDROMETHANOPTERINREDUC |
| | ID0087 | C | NITRO/FLAVIN REDUCTASE (EC 1.----). |
| 5 | ID0088 | C | Corynebacterium thermoaminogenes acn protein. |
| | ID0089 | C | HYPOTHETICAL 48.5 KDA PROTEIN. |
| | ID0090 | C | ISOCITRATE LYASE (EC 4.1.3.1). |
| | ID0091 | C | ARABINOSE OPERON PROTEIN ARAM. |
| | ID0092 | C | HYPOTHETICAL 48.1 KDA PROTEIN. |
| 10 | ID0093 | C | PHOSPHOENOLPYRUVATE CARBOXYKINASE. |
| | ID0094 | C | HMP (FLAVOHEMOGLOBIN). |
| | ID0095 | C | ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6). |
| | ID0096 | C | GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (GL |
| 15 | ID0097 | C | PUTATIVE MALOLACTIC ENZYME (EC 1.----) [INCLUDES: MALIC ENZ |
| | ID0098 | C | HYPOTHETICAL 27.9 KDA PROTEIN IN PHRC-GDH INTERGENIC REGION. |
| | ID0099 | C | FDRA PROTEIN. |
| 20 | ID0100 | C | ATP SYNTHASE GAMMA CHAIN. |
| | ID0101 | C | (PYRUVATE). |
| | ID0102 | C | DIHYDROLIPOYL TRANSACETYLASE AND LIPOAMIDE DEHYDROGENASE OF |
| | ID0103 | C | PROTOPORPHYRIN OXIDASE. |
| | ID0104 | C | PROBABLE PHOSPHATE BUTYRYLTRANSFERASE (EC 2.3.1.19) (PHOSPHOT |
| 25 | ID0105 | C | BH1977 PROTEIN. |
| | ID0106 | C | ASSIMILATORY NITRATE REDUCTASE ELECTRON TRANSFER SUBUNIT. |
| | ID0107 | C | ACONITATE HYDRATASE (EC 4.2.1.3) (CITRATE HYDRO- |
| 30 | LYASE) (ACON | | Arabidopsis aldehyde dehydrogenase (ALDH) -1. |
| | ID0108 | C | METHYLMALONATE-SEMALDEHYDE DEHYDROGENASE (EC 1.2.1.27) (METH |
| | ID0109 | C | PUTATIVE NAD(P)H NITROREDUCTASE YDFN (EC 1.----). |
| 35 | ID0110 | C | YTHB. |
| | ID0111 | C | NIFU-LIKE PROTEIN. |
| | ID0112 | C | ISOCITRATE LYASE. |
| | ID0113 | C | ALDEHYDE DEHYDROGENASE (ALDHT) (EC 1.2.1.3). |
| 40 | ID0114 | C | PUTATIVE DEHYDROGENASE SUBUNIT. |
| | ID0115 | C | ATTL. |
| | ID0116 | C | YTHA. |
| | ID0117 | C | PROBABLE NAD-DEPENDENT MALIC ENZYME (EC 1.1.1.38) (NAD-ME). |
| 45 | ID0118 | C | ORF starting with ATG of length 1209 |
| | ID0119 | C | HYPOTHETICAL 27.0 KDA PROTEIN IN SPOOA-MMGA |
| | ID0120 | C | INTERGENIC REGIO PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) (EC 4.1.1.49). |
| | ID0121 | C | CITRATE SYNTHASE-LIKE PROTEIN. |
| 50 | ID0122 | C | NITRATE REDUCTASE DELTA CHAIN (EC 1.7.99.4). |
| | ID0123 | C | ORF starting with ATG of length 1167 |
| | ID0124 | C | MALATE DEHYDROGENASE I (EC 1.1.1.37) (EC 1.1.1.82). |
| | ID0125 | C | 2-OXOGLUTARATE DEHYDROGENASE (FRAGMENT). |
| 55 | ID0126 | C | HYPOTHETICAL OXIDOREDUCTASE IN CSTA-AHPC INTERGENIC REGION. |
| | ID0127 | C | ORF starting with ATG of length 1134 |
| | ID0128 | C | YFHC PROTEIN. |
| | ID0129 | C | HYPOTHETICAL 49.2 KDA PROTEIN. |
| | ID0130 | C | GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE. |
| 60 | ID0131 | C | PROBABLE ALDEHYDE DEHYDROGENASE YWDH (EC 1.2.1.3). |
| | ID0132 | C | ALCOHOL-ACETALDEHYDE DEHYDROGENASE. |
| | ID0133 | C | ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) (ELEC |
| | ID0134 | C | PROBABLE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE YQIG (EC 1.---- |
| 65 | ID0135 | C | CYTOCHROME OXIDASE SUBUNIT II. |
| | ID0136 | C | |

| | | | |
|----|------------------------|-----|----------------------------------------------------------------|
| | ID0137 | C | ORF starting with ATG of length 854 |
| | ID0138 | C | PUTATIVE NAD(P)H NITROREDUCTASE YFKO (EC 1.---). |
| | ID0139 | C | PUTATIVE SECRETED HYDROLASE. |
| | ID0140 | C | SA0799 PROTEIN. |
| 5 | ID0141 | C | PUTATIVE NAD(P)H NITROREDUCTASE 12C (EC 1.---) |
| | (VEGETATIVE | | |
| | ID0142 | C | PUTATIVE ACYLPHOSPHATASE (EC 3.6.1.7) |
| | (ACYLPHOSPHATEPHOSPHOH | | |
| | ID0143 | C | Corynebacterium glutamicum MCT protein SEQ ID NO:544. |
| 10 | ID0144 | C | MANGANESE-DEPENDENT INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (P |
| | ID0145 | C | FOF1-ATP SYNTHASE EPSILON SUBUNIT. |
| | ID0146 | C | ORF starting with ATG of length 624 |
| 15 | ID0147 | C | ORF starting with ATG of length 615 |
| | ID0148 | C | GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD(P)+] (EC 1.1.1.94) (|
| | ID0149 | C | PUTATIVE FLAVODOXIN. |
| | ID0150 | C | PROBABLE FLAVODOXIN 2. |
| 20 | ID0151 | C | BH0367 PROTEIN. |
| | ID0152 | C | ELECTRON TRANSFER FLAVOPROTEIN (BETA SUBUNIT). |
| | ID0153 | C | ORF starting with ATG of length 555 |
| | ID0154 | C | HYPOTHETICAL 17.0 KDA PROTEIN. |
| | ID0155 | C | ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN). |
| 25 | ID0156 | C | ATP SYNTHASE B CHAIN. |
| | ID0157 | C | HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION. |
| | ID0158 | C | ACETOIN DEHYDROGENASE (TPP-DEPENDENT) ALPHA CHAIN. |
| 30 | ID0159 | C | HYPOTHETICAL 45.4 KDA PROTEIN IN SSPB-PRSA INTERGENIC REGION |
| | ID0160 | C | MENAQUINOL-CYTOCHROME C REDUCTASE CYTOCHROME B SUBUNIT. |
| | ID0161 | C | ORF starting with ATG of length 399 |
| 35 | ID0162 | C | MENAQUINOL-CYTOCHROME C REDUCTASE CYTOCHROME B/C SUBUNIT. |
| | ID0163 | C | ORF starting with ATG of length 330 |
| | ID0164 | C | ORF starting with ATG of length 294 |
| | ID0165 | C | ORF starting with ATG of length 225 |
| 40 | ID0166 | C | ORF starting with ATG of length 210 |
| | ID0167 | C | HYPOTHETICAL 50.9 KDA PROTEIN. |
| | ID0168 | CHR | YVCT PROTEIN. |
| | ID0169 | CHR | 376AA LONG HYPOTHETICAL DEHYDROGENASE. |
| | ID0170 | CP | YUFT PROTEIN. |
| 45 | ID0171 | CP | HYPOTHETICAL 52.1 KDA PROTEIN. |
| | ID0172 | CP | NADH DEHYDROGENASE SUBUNIT 5 (EC 1.6.5.3) (NADH-UBIQUINONEOX |
| | ID0173 | CR | ORF starting with ATG of length 803 |
| | ID0174 | D | CHROMOSOME PARTITION PROTEIN SMC. |
| | ID0175 | D | YUKA PROTEIN. |
| 50 | ID0176 | D | GLUCOSE INHIBITED DIVISION PROTEIN A. |
| | ID0177 | D | YHAN PROTEIN. |
| | ID0178 | D | STAGE III SPORULATION PROTEIN E. |
| | ID0179 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0180 | D | CELL DIVISION PROTEIN FTSZ. |
| 55 | ID0181 | D | HYPOTHETICAL 53.5 KDA PROTEIN IN SPOIIIE-HPT INTERGENIC REGION |
| | ID0182 | D | CELL DIVISION PROTEIN FTSZ. |
| | ID0183 | D | ROD SHAPE-DETERMINING PROTEIN MREB. |
| | ID0184 | D | MREBB PROTEIN. |
| 60 | ID0185 | D | MRP PROTEIN HOMOLOG. |
| | ID0186 | D | MREB-LIKE PROTEIN (MBL PROTEIN). |
| | ID0187 | D | PROTEIN GID. |
| | ID0188 | D | STAGE II SPORULATION PROTEIN D. |
| 65 | ID0189 | D | YTPT. |
| | ID0190 | D | CELL DIVISION PROTEIN FTSX HOMOLOG. |
| | ID0191 | D | SPOIIIE PROTEIN. |

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| | ID0192 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0193 | D | ORF starting with ATG of length 1990 |
| | ID0194 | D | HYPOTHETICAL 33.2 KDA PROTEIN IN FLHF-CHEB INTERGENIC |
| | REGION | | |
| 5 | ID0195 | D | CELL-DIVISION ATP-BINDING PROTEIN. |
| | ID0196 | D | MINICELL-ASSOCIATED PROTEIN DIVIVA. |
| | ID0197 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0198 | D | Neisseria meningitidis ORF 567 protein sequence SEQ |
| | ID NO:16 | | |
| 10 | ID0199 | D | ORF starting with ATG of length 1410 |
| | ID0200 | D | MAF PROTEIN. |
| | ID0201 | D | SEPTUM SITE-DETERMINING PROTEIN MINC. |
| | ID0202 | D | HYPOTHETICAL 43.3 KDA PROTEIN IN QOXD-VPR INTERGENIC |
| | REGION. | | |
| 15 | ID0203 | D | AMIDASE ENHANCER PRECURSOR (MODIFIER PROTEIN OF MAJOR |
| | AUTOLY | | |
| | ID0204 | D | SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION |
| | INHIBITO | | |
| 20 | ID0205 | D | HYPOTHETICAL 43.3 KDA PROTEIN IN QOXD-VPR INTERGENIC |
| | REGION. | | |
| | ID0206 | D | CAPSULAR POLYSACCHARIDE BIOSYNTHESIS. |
| | ID0207 | D | DIARRHEAL TOXIN. |
| | ID0208 | D | HYPOTHETICAL 13.9 KDA PROTEIN. |
| | ID0209 | D | HYPOTHETICAL PROTEIN HI1677. |
| 25 | ID0210 | D | CHROMOSOME PARTITION PROTEIN SMC. |
| | ID0211 | D | HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR. |
| | ID0212 | D | ORF starting with ATG of length 510 |
| | ID0213 | D | ORF starting with ATG of length 477 |
| | ID0214 | D | BH2986 PROTEIN. |
| 30 | ID0215 | D | ORF starting with ATG of length 417 |
| | ID0216 | D | Arabidopsis thaliana protein fragment SEQ ID NO: |
| | 42012. | | |
| | ID0217 | D | HYPOTHETICAL 43.3 KDA PROTEIN IN QOXD-VPR INTERGENIC |
| | REGION. | | |
| 35 | ID0218 | D | ORF starting with ATG of length 273 |
| | ID0219 | E | GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN (EC 1.4.1.13) |
| | (NADPH- | | |
| | ID0220 | E | 5-METHYLtetrahydrofolate S-HOMOCYSTEINE |
| | METHYLTRANSFERASE (EC | | |
| 40 | ID0221 | E | 5-METHYLtetrahydropteroyltriglutamate--HOMOCYSTEINE |
| | METHYLTR | | |
| | ID0222 | E | ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 3 (EC |
| | 6.3.5.4) | | |
| | ID0223 | E | PERMEASE. |
| 45 | ID0224 | E | PROBABLE PEPTIDASE YUXL (EC 3.4.21.-). |
| | ID0225 | E | PROBABLE GLYCINE DEHYDROGENASE [DECARBOXYLATING] |
| | SUBUNIT 2 (E | | |
| | ID0226 | E | HYPOTHETICAL 54.1 KDA PROTEIN IN DEOD-ARGE INTERGENIC |
| | REGION | | |
| 50 | ID0227 | E | ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 1 (EC |
| | 6.3.5.4) | | |
| | ID0228 | E | ARGININOSUCCINATE LYASE (EC 4.3.2.1) |
| | (ARGINOSUCCINASE) | | |
| | ID0229 | E | YBGF PROTEIN. |
| 55 | ID0230 | E | PROBABLE GLYCINE DEHYDROGENASE [DECARBOXYLATING] |
| | SUBUNIT 1 (E | | |
| | ID0231 | E | HYPOTHETICAL PROTEIN YWRD. |
| | ID0232 | E | Gamma glutamyl transpeptidase. |
| | ID0233 | E | YVBW PROTEIN. |
| 60 | ID0234 | E | PROBABLE ASPARTOKINASE (EC 2.7.2.4) (ASPARTATE |
| | KINASE). | | |
| | ID0235 | E | HOMOSERINE DEHYDROGENASE (EC 1.1.1.3) (HDH). |
| | ID0236 | E | YUSX PROTEIN. |
| | ID0237 | E | AMINO-ACID PERMEASE ROCE. |
| 65 | ID0238 | E | PUTATIVE L-AMINO ACID OXIDASE PRECURSOR. |
| | ID0239 | E | LEUCINE DEHYDROGENASE (EC 1.4.1.9) (LEUDH). |

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| | ID0240 | E | ACETYLORNITINE DEACETYLASE (YOKP). |
| | ID0241 | E | TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20). |
| | ID0242 | E | ORNITHINE CARBAMOYLTRANSFERASE, CATABOLIC (EC |
| 5 | 2.1.3.3) (OTCA | | |
| | ID0243 | E | YKBA PROTEIN. |
| | ID0244 | E | AMINOPEPTIDASE AMPS (EC 3.4.11.-). |
| | ID0245 | E | ORNITHINE AMINOTRANSFERASE (EC 2.6.1.13). |
| | ID0246 | E | CHORISMATE SYNTHASE (EC 4.6.1.4) (5- |
| | ENOLPYRUVYLSHIKIMATE-3-P | | |
| 10 | ID0247 | E | HYPOTHETICAL 39.7 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| | ID0248 | E | AMINO ACID CARRIER PROTEIN ALST. |
| | ID0249 | E | 2,4-DIAMINOBUTYRATE DECARBOXYLASE. |
| 15 | ID0250 | E | THREONINE SYNTHASE (EC 4.2.99.2). |
| | ID0251 | E | HISTIDINOL DEHYDROGENASE (EC 1.1.1.23) (HDH). |
| | ID0252 | E | CARBAMATE KINASE (EC 2.7.2.2). |
| | ID0253 | E | 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC |
| | 4.2.1.33) (IS | | |
| 20 | ID0254 | E | PEPTIDASE T (EC 3.4.11.-) (AMINOTRIPEPTIDASE) |
| | (TRIPEPTIDASE) | | |
| | ID0255 | E | PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH). |
| | ID0256 | E | NAD-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.2) |
| | (NAD-GDH). | | |
| 25 | ID0257 | E | ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE-- |
| | ASPARTA | | |
| | ID0258 | E | YBGH PROTEIN. |
| | ID0259 | E | YKVV PROTEIN. |
| | ID0260 | E | PUTATIVE AMINOTRANSFERASE B (EC 2.6.1.-). |
| | ID0261 | E | Peptide with glutamine synthetase activity. |
| 30 | ID0262 | E | YURG PROTEIN. |
| | ID0263 | E | ARGININE DEIMINASE (EC 3.5.3.6) (ARGININE |
| | DIHYDROLASE). | | |
| | ID0264 | E | THREONINE DEHYDRATASE (EC 4.2.1.16). |
| 35 | ID0265 | E | ASPARTOKINASE 2 (EC 2.7.2.4) (ASPARTOKINASE II) |
| | (ASPARTATE K | | |
| | ID0266 | E | YDFO PROTEIN. |
| | ID0267 | E | PUTATIVE PEPTIDASE IN GCVT-SPOIIIAA INTERGENIC REGION |
| | (EC 3. | | |
| 40 | ID0268 | E | PROBABLE AMINOMETHYLTRANSFERASE (EC 2.1.2.10) |
| | (GLYCINE CLEAV | | |
| | ID0269 | E | 2,4-DIAMINOBUTYRATE DECARBOXYLASE. |
| | ID0270 | E | HYPOTHETICAL TRANSPORT PROTEIN IN EXPZ-DINB |
| | INTERGENIC REGIO | | |
| 45 | ID0271 | E | PROBABLE CYSTEINE SYNTHASE (EC 4.2.99.8) (O- |
| | ACETYL SERINE SULF | | |
| | ID0272 | E | YJCJ PROTEIN. |
| | ID0273 | E | PROBABLE 4-AMINOBUTYRATE AMINOTRANSFERASE (EC |
| | 2.6.1.19) (GAM | | |
| 50 | ID0274 | E | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA |
| | REGION, | | |
| | ID0275 | E | PROJ. |
| | ID0276 | E | B. subtilis AnsB homologue. |
| | ID0277 | E | AROMATIC AMINO ACID TRANSPORTER. |
| | ID0278 | E | YFLA PROTEIN. |
| 55 | ID0279 | E | GLYCINE OXIDASE (EC 1.5.3.-). |
| | ID0280 | E | PUTATIVE INNER MEMBRANE PROTEIN. |
| | ID0281 | E | HYDANTOIN UTILIZATION PROTEIN A (ORF2). |
| | ID0282 | E | HYPOTHETICAL 38.3 KDA PROTEIN IN PEPT-KATB INTERGENIC |
| | REGION | | |
| 60 | ID0283 | E | HYPOTHETICAL 58.2 KDA PROTEIN IN KDG-T-XPT INTERGENIC |
| | REGION. | | |
| | ID0284 | E | HYPOTHETICAL 43.4 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| 65 | ID0285 | E | GLYCINE BETAINE TRANSPORT SYSTEM PERMEASE PROTEIN |
| | OPUAB. | | |
| | ID0286 | E | TIORF195 PROTEIN. |

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| | ID0287 | E | HOMOSERINE KINASE (EC 2.7.1.39) (HK). |
| | ID0288 | E | YRVO PROTEIN. |
| | ID0289 | E | PZ-PEPTIDASE. |
| 5 | ID0290 | E | TARTRATE DEHYDROGENASE. |
| | ID0291 | E | CYSTATHIONINE GAMMA-LYASE. |
| | ID0292 | E | ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (AS). |
| | ID0293 | E | DIPEPTIDE TRANSPORT PROTEIN DPPA. |
| 10 | ID0294 | E | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH). |
| | ID0295 | E | PROBABLE AMINO-ACID ABC TRANSPORTER ATP-BINDING PROTEIN YCKI. |
| | ID0296 | E | YNGG PROTEIN. |
| 15 | ID0297 | E | PUTATIVE HYDANTOIN UTILIZATION PROTEIN. |
| | ID0298 | E | HISTIDINOL-PHOSPHATE AMINOTRANSFERASE/TYROSINE AND PHENYLALALA. |
| | ID0299 | E | BUSAA. |
| | ID0300 | E | L-2,4-DIAMINOBUTYRATE DECARBOXYLASE (EC 4.1.1.). |
| 20 | ID0301 | E | ANTHRAHALATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18). |
| | ID0302 | E | HISF PROTEIN (CYCLASE). |
| | ID0303 | E | N-ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11). |
| | ID0304 | E | YURW PROTEIN. |
| | ID0305 | E | 2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12). |
| | ID0306 | E | PROBABLE AMINO-ACID ABC TRANSPORTER EXTRACELLULAR BINDING PR. |
| 25 | ID0307 | E | L-SERINE DEHYDRATASE ALPHA SUBUNIT. |
| | ID0308 | E | Bacillus subtilis metalloprotease YurH. |
| | ID0309 | E | PROBABLE ABC TRANSPORTER EXTRACELLULAR BINDING PROTEIN YCKB. |
| 30 | ID0310 | E | YNBB. |
| | ID0311 | E | HYPOTHETICAL 57.1 KDA PROTEIN. |
| | ID0312 | E | LYSINE DECARBOXYLASE (EC 4.1.1.18) (LDC). |
| | ID0313 | E | HYPOTHETICAL 53.2 KDA PROTEIN IN XPAC-ABRB INTERGENIC REGION. |
| 35 | ID0314 | E | OLIGOENDOPEPTIDASE F HOMOLOG (EC 3.4.24.-). |
| | ID0315 | E | SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) (SERINE METHYL). |
| | ID0316 | E | PUTATIVE AMINOTRANSFERASE A (EC 2.6.1.-). |
| 40 | ID0317 | E | ORF starting with ATG of length 2001. |
| | ID0318 | E | GLYCINE BETAINE/CARNITINE/CHOLINE TRANSPORT SYSTEM PERMEASE. |
| | ID0319 | E | TRANSCARBAMYLASE. |
| | ID0320 | E | SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25). |
| 45 | ID0321 | E | COME OPERON PROTEIN 4. |
| | ID0322 | E | ORF starting with ATG of length 1971. |
| | ID0323 | E | Bacillus subtilis Class II EPSPS. |
| | ID0324 | E | PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTID. |
| | ID0325 | E | SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT). |
| 50 | ID0326 | E | GLYCINE BETAINE/CARNITINE/CHOLINE TRANSPORT SYSTEM PERMEASE. |
| | ID0327 | E | GLUTAMYL ENDOPEPTIDASE PRECURSOR (EC 3.4.21.19) (GLUTAMATE S). |
| | ID0328 | E | ASPARTOKINASE 1 (EC 2.7.2.4) (ASPARTOKINASE I) (ASPARTATE KI). |
| 55 | ID0329 | E | BH0994 PROTEIN. |
| | ID0330 | E | HYPOTHETICAL 40.8 KDA PROTEIN IN PCP-LMRB INTERGENIC REGION. |
| | ID0331 | E | HYPOTHETICAL 39.4 KDA OXIDOREDUCTASE IN HOM-MRGA. |
| 60 | INTERGENIC | | CYSTEINE SYNTHASE. |
| | ID0332 | E | 3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33) (IS). |
| | ID0333 | E | IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19) (IGPD). |

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| | ID0335 (ASA DEHY | E | ASPARTATE-SEMALDEHYDE DEHYDROGENASE (EC 1.2.1.11) |
| | ID0336 | E | YBEC PROTEIN (ORF3). |
| 5 | ID0337 | E | GLYCINE BETAINE-BINDING PROTEIN PRECURSOR. |
| | ID0338 | E | ORF starting with ATG of length 1797 |
| | ID0339 | E | 3-ISOPROPYLALATE DEHYDROGENASE (EC 1.1.1.85) (BETA- |
| | IPM DEHY | | |
| | ID0340 | E | PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN |
| | YCKA. | | |
| 10 | ID0341 | E | ORF starting with ATG of length 1740 |
| | ID0342 (NADPH- | E | GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN (EC 1.4.1.13) |
| | ID0343 | E | PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOLOG 1. |
| | ID0344 | E | ALANINE DEHYDROGENASE (EC 1.4.1.1) (STAGE V |
| 15 | SPORULATION PROT | | |
| | ID0345 | E | HISTIDINE BIOSYNTHESIS BIFUNCTIONAL PROTEIN HISIE |
| | [INCLUDES: | | |
| | ID0346 | E | NIFS2. |
| 20 | ID0347 (AGK) (N-AC | E | ACETYLGLUTAMATE KINASE (EC 2.7.2.8) (NAG KINASE) |
| | ID0348 | E | BH1629 PROTEIN. |
| | ID0349 | E | HYPOTHETICAL 27.6 KDA LIPOPROTEIN IN NUCB-AROD |
| | INTERGENIC RE | | |
| | ID0350 | E | HYPOTHETICAL TRANSPORT PROTEIN IN NDHF-CSGA |
| 25 | INTERGENIC REGIO | | |
| | ID0351 | E | BH0591 PROTEIN. |
| | ID0352 | E | ALANINE DEHYDROGENASE (STAGE V SPORULATION PROTEIN N) |
| | (EC 1. | | |
| 30 | ID0353 | E | 5-METHYLtetrahydrofolate S-HOMOCYSTEINE |
| | METHYLTRANSFERASE (EC | | |
| | ID0354 | E | BRANCH-CHAIN AMINO ACID TRANSPORTER. |
| | ID0355 | E | HYPOTHETICAL 63.8 KDA PROTEIN IN SIPU-PBPC INTERGENIC |
| | REGION | | |
| | ID0356 | E | B. subtilis hydrolase protein YTMA. |
| 35 | ID0357 | E | ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17). |
| | ID0358 | E | AMINO ACID TRANSPORTER. |
| | ID0359 | E | Alanine dehydrogenase amino acid sequence. |
| | ID0360 | E | YEST PROTEIN. |
| 40 | ID0361 | E | HYPOTHETICAL 69.3 KDA PROTEIN. |
| | ID0362 | E | 314AA LONG HYPOTHETICAL CARBAMATE KINASE (FUCOXANTHIN |
| | CHLORO | | |
| | ID0363 | E | YEBA. |
| | ID0364 | E | AMIDOTRANSFERASE HISH (EC 2.4.2.-). |
| 45 | ID0365 | E | PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOLOG 2. |
| | ID0366 | E | YCGF PROTEIN. |
| | ID0367 | E | HYPOTHETICAL 28.9 KDA PROTEIN IN ILVA 3'REGION. |
| | ID0368 | E | ORF starting with ATG of length 1512 |
| | ID0369 | E | GAMMA-GLUTAMYL PHOSPHATE REDUCTASE. |
| | ID0370 | E | SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE |
| 50 | AMINOPROPYLTRA | | |
| | ID0371 | E | AMINO ACID CARRIER PROTEIN. |
| | ID0372 | E | AMINO ACID TRANSPORTER. |
| | ID0373 | E | ORF starting with ATG of length 1404 |
| | ID0374 | E | ORF starting with ATG of length 1404 |
| 55 | ID0375 (GLUTAMAT | E | NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4) |
| | BINDING PR | | |
| | ID0376 | E | PROBABLE AMINO-ACID ABC TRANSPORTER EXTRACELLULAR |
| 60 | ID0377 REGION | E | HYPOTHETICAL 30.2 KDA PROTEIN IN HTRA-DPPA INTERGENIC |
| | ID0378 | E | YJCI PROTEIN. |
| | ID0379 | E | DIAMINOBUTYRATE--PYRUVATE AMINOTRANSFERASE (EC |
| | 2.6.1.76) (L- | | |
| | ID0380 | E | VALINE-PYRUVATE AMINOTRANSFERASE. |
| 65 | ID0381 1.2.1.38) (A | E | N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC |

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| | ID0382 | E | BH3963 PROTEIN. |
| | ID0383 | E | HYPOTHETICAL 23.6 KDA PROTEIN IN KIPR-PBPC INTERGENIC |
| | REGION | | |
| 5 | ID0384 | E | Region of tryptophan synthase A. |
| | ID0385 | E | ARGININE DEIMINASE (EC 3.5.3.6) (ARGININE |
| | DIHYDROLASE). | | |
| | ID0386 | E | PROBABLE L-SERINE DEHYDRATASE, BETA CHAIN (EC |
| | 4.2.1.13) (L-S | | |
| 10 | ID0387 | E | DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26) (DHPR). |
| | ID0388 | E | RHBA DIAMINOBUTYRATE-PYRUVATE AMINOTRANSFERASE |
| | (EC2.6.1.46). | | |
| | ID0389 | E | SHIKIMATE KINASE (EC 2.7.1.71) (SK). |
| | ID0390 | E | Neisseria gonorrhoeae ORF 705 protein sequence SEQ ID |
| | NO:2358 | | |
| 15 | ID0391 | E | YFLA PROTEIN. |
| | ID0392 | E | HOMOSERINE O-SUCCINYLTRANSFERASE (EC 2.3.1.46) |
| | (HOMOSERINE O | | |
| | ID0393 | E | SODIUM/ALANINE SYMPORTER. |
| | ID0394 | E | 376AA LONG HYPOTHETICAL DEHYDROGENASE. |
| 20 | ID0395 | E | 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC |
| | 4.2.1.33) (IS | | |
| | ID0396 | E | HYPOTHETICAL 32.4 KDA PROTEIN. |
| | ID0397 | E | ORF starting with ATG of length 1104 |
| | ID0398 | E | THERMOSTABLE DIPEPTIDASE BDP. |
| 25 | ID0399 | E | 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3- |
| | DEHYDROQUINASE | | |
| | ID0400 | E | ORF starting with ATG of length 1020 |
| | ID0401 | E | UGPC. |
| 30 | ID0402 | E | HYPOTHETICAL 14.8 KDA PROTEIN IN TDK-PRFA INTERGENIC |
| | REGION. | | |
| | ID0403 | E | HYPOTHETICAL 23.4 KDA PROTEIN IN AAPA-SIGV INTERGENIC |
| | REGION | | |
| | ID0404 | E | Arabidopsis thaliana protein fragment SEQ ID NO: |
| | 18888. | | |
| 35 | ID0405 | E | ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 1 (EC |
| | 6.3.5.4) | | |
| | ID0406 | E | N- (5'-PHOSPHORIBOSYL) ANTHRANILATE ISOMERASE (EC |
| | 5.3.1.24) (P | | |
| 40 | ID0407 | E | INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE. |
| | ID0408 | E | AROA(G) PROTEIN [INCLUDES: PHOSPHO-2-DEHYDRO-3- |
| | DEOXYHEPTONAT | | |
| | ID0409 | E | BH1818 PROTEIN. |
| | ID0410 | E | D-ALANINE GLYCINE PERMEASE. |
| | ID0411 | E | ORF starting with ATG of length 906 |
| 45 | ID0412 | E | YNDN PROTEIN. |
| | ID0413 | E | PUTATIVE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1). |
| | ID0414 | E | HYPOTHETICAL 53.2 KDA PROTEIN IN XPAC-ABRB INTERGENIC |
| | REGION | | |
| 50 | ID0415 | E | ORF starting with ATG of length 870 |
| | ID0416 | E | HOMOSERINE KINASE (EC 2.7.1.39) (HK). |
| | ID0417 | E | PROBABLE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) |
| | (3-DEHYD | | |
| | ID0418 | E | ASPARTOKINASE II ALPHA AND BETA SUBUNITS (EC |
| | 2.7.2.4). | | |
| 55 | ID0419 | E | 5-ENOLPYRUVYLSHIKMATE 3-P SYNTHASE (FRAGMENT). |
| | ID0420 | E | HYPOTHETICAL 61.8 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| | ID0421 | E | YKCA PROTEIN. |
| 60 | ID0422 | E | ORF starting with ATG of length 801 |
| | ID0423 | E | GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA |
| | LIGASE | | |
| | ID0424 | E | HYPOTHETICAL 14.4 KDA PROTEIN IN TETB-EXOA INTERGENIC |
| | REGION | | |
| 65 | ID0425 | E | Arabidopsis thaliana protein fragment SEQ ID NO: |
| | 12719. | | |
| | ID0426 | E | ORF starting with ATG of length 1431 |

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| | ID0427 | E | HYPOTHETICAL 14.4 KDA PROTEIN IN EPR-GALK INTERGENIC |
| | REGION. | | |
| | ID0428 | E | HYPOTHETICAL 15.2 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| 5 | ID0429 | E | 3-DEHYDROQUINATE SYNTHASE (EC 4.6.1.3). |
| | ID0430 | E | YDAO PROTEIN. |
| | ID0431 | E | ORF starting with ATG of length 654 |
| | ID0432 | E | ORF starting with ATG of length 617 |
| | ID0433 | E | YUSH PROTEIN. |
| 10 | ID0434 | E | ORF starting with ATG of length 573 |
| | ID0435 | E | DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP |
| | DECARBOXYLA | | |
| | ID0436 | E | YKRV PROTEIN. |
| | ID0437 | E | ORF starting with ATG of length 536 |
| 15 | ID0438 | E | MALTOSE PERMEASE (MALA). |
| | ID0439 | E | ORF starting with TTG or GTG of length 1038 |
| | ID0440 | E | METAL-ACTIVATED PYRIDOXAL ENZYME. |
| | ID0441 | E | Staphylococcus aureus mutant P7C18 virulence gene |
| | product. | | |
| 20 | ID0442 | E | CYSTEINE SYNTHASE A (EC 4.2.99.8). |
| | ID0443 | E | BRANCHED-CHAIN AMINO ACID TRANSPORTER. |
| | ID0444 | E | ORF starting with ATG of length 465 |
| | ID0445 | E | YDAO PROTEIN. |
| 25 | ID0446 | E | 3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95). |
| | ID0447 | E | NITROGEN REGULATORY PROTEIN P-II (GLNB-2). |
| | ID0448 | E | GLYCINE CLEAVAGE SYSTEM PROTEIN H (AMINOMETHYL |
| | CARRIER). | | |
| | ID0449 | E | Human ORFX ORF544 polypeptide sequence SEQ ID |
| | NO:1088. | | |
| 30 | ID0450 | E | 307AA LONG HYPOTHETICAL PHOSPHOGLYCERATE |
| | DEHYDROGENASE. | | |
| | ID0451 | E | ORF starting with ATG of length 387 |
| | ID0452 | E | ORF starting with ATG of length 837 |
| 35 | ID0453 | E | ORF starting with ATG of length 360 |
| | ID0454 | E | YEBA. |
| | ID0455 | E | PROBABLE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) |
| | (3-DEHYD | | |
| | ID0456 | E | BH3810 PROTEIN. |
| | ID0457 | E | ORF starting with ATG of length 321 |
| 40 | ID0458 | E | AMINO ACID CARRIER PROTEIN. |
| | ID0459 | E | Human ORFX ORF618 polypeptide sequence SEQ ID |
| | NO:1236. | | |
| | ID0460 | E | HYPOTHETICAL PROTEIN XF2305. |
| | ID0461 | E | AGAE. |
| 45 | ID0462 | E | ORF starting with ATG of length 237 |
| | ID0463 | E | ORF starting with ATG of length 237 |
| | ID0464 | E | ORF starting with ATG of length 231 |
| | ID0465 | E | HOMOCITRATE SYNTHASE (EC 4.1.3.21). |
| 50 | ID0466 | E | ORF starting with ATG of length 225 |
| | ID0467 | E | ORF starting with ATG of length 225 |
| | ID0468 | E | YNDN PROTEIN. |
| | ID0469 | E | YEST PROTEIN. |
| | ID0470 | E | BH1818 PROTEIN. |
| 55 | ID0471 | E | HISF PROTEIN (CYCLASE). |
| | ID0472 | EF | CARBAMOYL-PHOSPHATE SYNTHETASE (CATALYTIC SUBUNIT). |
| | ID0473 | EF | CARBAMOYL-PHOSPHATE SYNTHASE, ARGININE-SPECIFIC, |
| | LARGE CHAIN | | |
| | ID0474 | EF | CARBAMOYL-PHOSPHATE SYNTHASE, PYRIMIDINE-SPECIFIC, |
| 60 | ID0475 | EF | ORF starting with ATG of length 3213 |
| | ID0476 | EF | CARBAMOYLPHOSPHATE SYNTHETASE HEAVY SUBUNIT. |
| | ID0477 | EF | CARBAMOYL-PHOSPHATE SYNTHASE, ARGININE-SPECIFIC, |
| | SMALL CHA | | |
| | ID0478 | EF | GLUTAMINE-DEPENDENT CARBAMOYL PHOSPHATE SYNTHASE (EC |
| 65 | 6.3.5.5 | | |

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| | ID0479 | EH | PROBABLE MALONIC SEMIALDEHYDE OXIDATIVE DECARBOXYLASE |
| | (EC 1. | | |
| | ID0480 | EH | YDAP PROTEIN. |
| | ID0481 | EH | B. subtilis acetohydroxyacid synthetase subunit, |
| 5 | IlvB. | | |
| | ID0482 | EH | PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-) |
| | (ADC SY | | |
| | ID0483 | EH | KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86) |
| | (ACETOHYDROXY-ACID | | |
| 10 | ID0484 | EH | ALPHA-ACETOLACTATE SYNTHASE PROTEIN, ALSS. |
| | ID0485 | EH | PHOSPHOADENOSE PHOSPHOSULFATE REDUCTASE (EC |
| | 1.8.99.4) (PAP | | |
| | ID0486 | EH | ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27). |
| | ID0487 | EH | PROBABLE PHOSPHOADENOSE PHOSPHOSULFATE REDUCTASE |
| 15 | (EC 1.8.9 | | |
| | ID0488 | EH | 4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-) (ADC |
| | LYASE) (AD | | |
| | ID0489 | EH | PARA-AMINOBENZOATE/ANTHRANILATE SYNTHASE GLUTAMINE |
| | AMIDOTRAN | | |
| 20 | ID0490 | EH | ORF starting with ATG of length 1746 |
| | ID0491 | EH | ANTHRANILATE SYNTHASE. |
| | ID0492 | EH | PUTATIVE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE |
| | (EC 2.6. | | |
| | ID0493 | EH | ORF starting with ATG of length 1539 |
| 25 | ID0494 | EH | D-ALANINE AMINOTRANSFERASE. |
| | ID0495 | EH | B. subtilis IlvE homologue #1. |
| | ID0496 | EHR | HYPOTHETICAL 55.0 KDA PROTEIN IN EPR-GALK INTERGENIC |
| | REGION. | | |
| | ID0497 | EHR | NA+/MYO-INOSITOL COTRANSPORTER. |
| 30 | ID0498 | EHR | HYPOTHETICAL 40.1 KDA PROTEIN IN SIPU-KIPI INTERGENIC |
| | REGION | | |
| | ID0499 | EHR | YOLC. |
| | ID0500 | EHR | OSMOREGULATED PROLINE TRANSPORTER (SODIUM/PROLINE |
| | SYMPORTER) | | |
| 35 | ID0501 | EHR | Mouse high affinity choline transporter protein. |
| | ID0502 | EHR | HOMOLOGUE OF PROLINE PERMEASE OF E. COLI. |
| | ID0503 | EHR | HOMOLOGUE OF PROLINE PERMEASE OF E. COLI. |
| | ID0504 | EHR | HOMOLOGUE OF PROLINE PERMEASE OF E. COLI. |
| | ID0505 | EJ | L-ASPARAGINASE (EC 3.5.1.1) (L-ASPARAGINE |
| | AMIDOHYDROLASE). | | |
| | ID0506 | EJ | L-ASPARAGINASE. |
| | ID0507 | EM | PROBABLE 5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC |
| 40 | 4.2.1.41 | | |
| | ID0508 | EM | DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS) |
| 45 | (VEGETATI | | |
| | ID0509 | EM | DIHYDRODIPICOLINATE SYNTHASE. |
| | ID0510 | EM | DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS) |
| | (VEGETATI | | |
| | ID0511 | EM | ORF starting with ATG of length 606 |
| 50 | ID0512 | EP | OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR. |
| | ID0513 | EP | B. subtilis oppD ATPase. |
| | ID0514 | EP | DIPEPTIDE-BINDING PROTEIN DPPE PRECURSOR. |
| | ID0515 | EP | OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN APPF. |
| | ID0516 | EP | DIPEPTIDE TRANSPORTER PROTEIN DPPA (FRAGMENT). |
| 55 | ID0517 | EP | OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN APPD. |
| | ID0518 | EP | OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN APPB. |
| | ID0519 | EP | OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN APPC. |
| | ID0520 | EP | YKFD. |
| | ID0521 | EP | OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC. |
| 60 | ID0522 | EP | DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC. |
| | ID0523 | EP | DIPEPTIDE ABC TRANSPORTER (PERMEASE). |
| | ID0524 | EP | B. subtilis oppA ligand binding protein. |
| | ID0525 | EP | NICKEL TRANSPORT SYSTEM (PERMEASE). |
| | ID0526 | EP | NICKEL TRANSPORT SYSTEM (PERMEASE). |
| 65 | ID0527 | EP | NICKEL ABC TRANSPORTER (PERMEASE). |
| | ID0528 | EP | DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC. |

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| | ID0529 | EP | DIPEPTIDE TRANSPORT ATP-BINDING PROTEIN DPPD. |
| | ID0530 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0531 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0532 | EP | OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN AMIF. |
| 5 | ID0533 | EP | NICKEL ABC TRANSPORTER (PERMEASE). |
| | ID0534 | EP | NICKEL ABC TRANSPORTER (NICKEL-BINDING PROTEIN). |
| | ID0535 | EP | OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPB. |
| | ID0536 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0537 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 10 | ID0538 | EP | DIPEPTIDE TRANSPORTER DPPD HOMOLOG. |
| | ID0539 | EP | B. subtilis oppB membrane protein. |
| | ID0540 | EP | 420AA LONG HYPOTHETICAL OLIGOPEPTIDE TRANSPORT ATP- |
| | BINDING P | | |
| | ID0541 | EP | B. subtilis oppA ligand binding protein. |
| 15 | ID0542 | EP | ATPASE OPPD. |
| | ID0543 | EP | ORF starting with ATG of length 240 |
| | ID0544 | EP | ORF starting with ATG of length 213 |
| | ID0545 | EP | ORF starting with ATG of length 210 |
| | ID0546 | ER | HYPOTHETICAL 64.1 KDA PROTEIN. |
| 20 | ID0547 | ER | GLUTAMATE SYNTHASE (EC 1.4.1.13) (GLUTAMATE SYNTHASE (NADPH)) |
| | ID0548 | ER | YTVP. |
| | ID0549 | ER | NAD ALCOHOL DEHYDROGENASE. |
| | ID0550 | ER | Pyrococcus horikoshii thermophilic dehydrogenase. |
| 25 | ID0551 | ER | L-IDITOL 2-DEHYDROGENASE (EC 1.1.1.14). |
| | ID0552 | ER | ZINC-CONTAINING ALCOHOL DEHYDROGENASE. |
| | ID0553 | ER | ORF starting with ATG of length 1140 |
| | ID0554 | ER | ORF starting with ATG of length 321 |
| | ID0555 | F | YFKN PROTEIN. |
| 30 | ID0556 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (EC 6.3.5.3) (|
| | ID0557 | F | HYPOTHETICAL 132.7 KDA PROTEIN IN CSPB-GLPP |
| | INTERGENIC REGIO | | |
| | ID0558 | F | RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4. |
| 35 | ID0559 | F | GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2) (GLUTAMINE |
| | ID0560 | F | BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH [INCLUDES: PHOS |
| 40 | ID0561 | F | TRANSFERASE (GLUTAMINE AMIDOTRANSFERASE) |
| | ID0562 | F | ADENYLOSUCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL) |
| | ID0563 | F | ADENINE DEAMINASE (EC 3.5.4.2) (ADENASE) (ADENINE AMINASE). |
| 45 | ID0564 | F | HYPOTHETICAL 66.6 KDA PROTEIN IN PURD-PCRB INTERGENIC REGION |
| | ID0565 | F | PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GL |
| | ID0566 | F | DIHYDROOROTASE (EC 3.5.2.3) (DHOASE). |
| 50 | ID0567 | F | PYRIMIDINE NUCLEOSIDE TRANSPORT PROTEIN. |
| | ID0568 | F | URACIL PERMEASE (URACIL TRANSPORTER). |
| | ID0569 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE |
| | SUBUNIT (EC | | |
| | ID0570 | F | ORF starting with ATG of length 2985 |
| 55 | ID0571 | F | HYPOTHETICAL 43.7 KDA PROTEIN IN PEPT-KATB INTERGENIC REGION |
| | ID0572 | F | DIHYDROORotate DEHYDROGENASE, CATALYTIC SUBUNIT (EC 1.3.3.1) |
| | ID0573 | F | PUTATIVE PURINE PERMEASE YWDJ. |
| 60 | ID0574 | F | ALLANTOINASE (EC 3.5.2.5). |
| | ID0575 | F | A formate transport associated protein, PurU. |
| | ID0576 | F | CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHET |
| | ID0577 | F | IMPDH. |
| 65 | ID0578 | F | PYRIMIDINE NUCLEOSIDE PHOSPHORYLASE. |
| | ID0579 | F | YJBT PROTEIN. |

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| | ID0580 | F | YJBT PROTEIN. |
| | ID0581 | F | PURINE NUCLEOSIDE PHOSPHORYLASE I (EC 2.4.2.1) (PNP |
| | I) (PU-N | | |
| | ID0582 | F | XANTHINE PERMEASE. |
| 5 | ID0583 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE |
| | SYNTHASE (EC | | |
| | ID0584 | F | SA2078 PROTEIN. |
| | ID0585 | F | RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE BETA CHAIN (EC |
| 10 | 1.17.4.1 | | |
| | ID0586 | F | MTA/SAH NUCLEOSIDASE [INCLUDES: 5'- |
| | METHYLTHIOADENOSINE NUCLE | | |
| | ID0587 | F | DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4) |
| | (PHOSPHODEOXYRIB | | |
| 15 | ID0588 | F | ORF starting with ATG of length 1776 |
| | ID0589 | F | ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP |
| | TRANSPHOSPHORYLASE) (S | | |
| | ID0590 | F | CYTIDYLATE KINASE (EC 2.7.4.14) (CK) (CYTIDINE |
| | MONOPHOSPHATE | | |
| 20 | ID0591 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC |
| | 6.3.3.1) | | |
| | ID0592 | F | COME OPERON PROTEIN 2. |
| | ID0593 | F | FORMYLtetrahydrofolate SYNTHETASE. |
| | ID0594 | F | OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10) |
| | (OPRT) (OPRT | | |
| 25 | ID0595 | F | YUND PROTEIN. |
| | ID0596 | F | ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) |
| | (APRT) . | | |
| | ID0597 | F | ASPARTATE TRANSCARBAMOYLASE. |
| 30 | ID0598 | F | HYPOTHETICAL 24.1 KDA PROTEIN IN SERS-DNAZ INTERGENIC |
| | REGION | | |
| | ID0599 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHETASE I. |
| | ID0600 | F | XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.-). |
| | ID0601 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC |
| | SUBUNIT (E | | |
| 35 | ID0602 | F | HYPOTHETICAL 25.4 KDA PROTEIN IN SERS-DNAZ INTERGENIC |
| | REGION | | |
| | ID0603 | F | THYMIDINE KINASE (EC 2.7.1.21) . |
| | ID0604 | F | Thymidylate kinase-2. |
| | ID0605 | F | URIDYLATE KINASE (EC 2.7.4.-) (UK) (URIDINE |
| 40 | MONOPHOSPHATE KI | | |
| | ID0606 | F | ORF starting with ATG of length 1146 |
| | ID0607 | F | C-1-TETRAHYDROFOLATE SYNTHASE, MITOCHONDRIAL |
| | PRECURSOR (C1-T | | |
| 45 | ID0608 | F | PurR protein sequence. |
| | ID0609 | F | URIDINE KINASE (EC 2.7.1.48) (URIDINE |
| | MONOPHOSPHOKINASE) . | | |
| | ID0610 | F | XANTHINE PERMEASE. |
| | ID0611 | F | Nucleoside phosphorylase. |
| | ID0612 | F | DEOXYRIBOSE-PHOSPHATE ALDOLASE. |
| 50 | ID0613 | F | THYMIDYLATE SYNTHASE A (EC 2.1.1.45) (TS A) (TSASE |
| | A) . | | |
| | ID0614 | F | ORF starting with ATG of length 870 |
| | ID0615 | F | YUND PROTEIN. |
| | ID0616 | F | Corynebacterium glutamicum MP protein sequence SEQ ID |
| 55 | NO:948 | | |
| | ID0617 | F | PYRIMIDINE OPERON REGULATORY PROTEIN PYRR. |
| | ID0618 | F | NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6) (NDK) (NDP |
| | KINASE | | |
| | ID0619 | F | PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC |
| 60 | 2.1.2.2) (GA | | |
| | ID0620 | F | CYTIDINE DEAMINASE (EC 3.5.4.5) . |
| | ID0621 | F | ORF starting with ATG of length 591 |
| | ID0622 | F | THYMIDYLATE SYNTHASE A (EC 2.1.1.45) (TS A) (TSASE |
| | A) . | | |
| 65 | ID0623 | F | HYPOTHETICAL 9.7 KDA PROTEIN IN PURC-PURL INTERGENIC |
| | REGION. | | |

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| | ID0624 | F | PUTATIVE ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4). |
| | ID0625 | F | GUANYLATE KINASE (EC 2.7.4.8) (GMP KINASE). |
| | ID0626 | F | Zea mays protein fragment SEQ ID NO: 40074. |
| 5 | ID0627 | F | Corynebacterium glutamicum MP protein sequence SEQ ID NO: 998. |
| | ID0628 | F | GARS-AIRS-GART (FRAGMENT). |
| | ID0629 | F | PURINE NUCLEOSIDE PHOSPHORYLASE II (EC 2.4.2.1) (PNP II) (PU). |
| 10 | ID0630 | F | PHOSPHORIBOSYLGlycinamide FORMYLTRANSFERASE (EC 2.1.2.2) (GA). |
| | ID0631 | F | ORF starting with ATG of length 261. |
| | ID0632 | F | DIHYDROOROTASE (EC 3.5.2.3) (DHOASE). |
| | ID0633 | FE | RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) (PHOSPHORIBO). |
| 15 | ID0634 | FE | PRPP SYNTHETASE (EC 2.7.6.1). |
| | ID0635 | FGR | HIT PROTEIN. |
| | ID0636 | FGR | HYPOTHETICAL HIT-LIKE PROTEIN MJ0866. |
| | ID0637 | FH | HYPOTHETICAL 54.0 KDA PROTEIN IN NRGA-USD INTERGENIC REGION. |
| 20 | ID0638 | FH | HYPOTHETICAL 54.0 KDA PROTEIN IN NRGA-USD INTERGENIC REGION. |
| | ID0639 | FJ | HYPOTHETICAL 17.8 KDA PROTEIN IN SERS-DNAH INTERGENIC REGION. |
| | ID0640 | FJ | YKOA. |
| 25 | ID0641 | FR | BH0185 PROTEIN. |
| | ID0642 | G | PEP SYNTHASE. |
| | ID0643 | G | GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1). |
| | ID0644 | G | Bacillus species alpha-glucosidase. |
| | ID0645 | G | LEVANASE PRECURSOR (EC 3.2.1.65) (2,6-BETA-D- |
| 30 | FRUCTANFRUCTANO | | |
| | ID0646 | G | CHITINASE. |
| | ID0647 | G | PEP SYNTHASE. |
| | ID0648 | G | PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (EC 2.7.3.9) (|
| 35 | ID0649 | G | GLUCOSIDASE. |
| | ID0650 | G | Arabinose isomerase from Bacillus licheniformis, |
| | deduced amo | | |
| | ID0651 | G | YESZ PROTEIN. |
| | ID0652 | G | HYPOTHETICAL 88.3 KDA PROTEIN IN CLPP-CRH INTERGENIC |
| 40 | ID0653 | G | 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18). |
| | (GLYCOGEN BR | | |
| | ID0654 | G | HYPOTHETICAL 68.9 KDA PROTEIN. |
| | ID0655 | G | Bacillus sp. exo-alpha-1,4-glucosidase, AMY1084 |
| 45 | ID0656 | G | HYPOTHETICAL 79.2 KDA PROTEIN. |
| | ID0657 | G | TREHALOSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.93). |
| | (ALPHA, ALPHA-P | | |
| | ID0658 | G | 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING II (EC 1.1 |
| 50 | ID0659 | G | HYPOTHETICAL 70.6 KDA LIPOPROTEIN IN FEUA-SIGW |
| | INTERGENIC RE | | |
| | ID0660 | G | BETA-D-GALACTOSIDASE. |
| | ID0661 | G | CHITINASE PRECURSOR (EC 3.2.1.14). |
| | ID0662 | G | GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9). |
| 55 | (PHOSPHOGLU | | |
| | ID0663 | G | LIPOPROTEIN LPLA PRECURSOR. |
| | ID0664 | G | ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE |
| | DEHYDRATASE) (2-PH | | |
| 60 | ID0665 | G | Amino acid sequence of a Staphylococcus aureus tktA polypept. |
| | ID0666 | G | GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) (G6PD) (VE |
| | ID0667 | G | XYLOSE ISOMERASE (EC 5.3.1.5). |
| | ID0668 | G | PROBABLE BETA-GLUCOSIDASE (EC 3.2.1.21) (GENTIOBIASE) (CELLO |
| 65 | ID0669 | G | PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM). |

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| | ID0670 | G | HYPOTHETICAL 48.5 KDA PROTEIN. |
| | ID0671 | G | GLUCAN-GLUCOHYDROLASE (EC 3.2.1.74) (GLUCAN 1,4-BETA- |
| | GLUCOSI | | |
| | ID0672 | G | YDHP PROTEIN. |
| 5 | ID0673 | G | HYPOTHETICAL 47.3 KDA PROTEIN. |
| | ID0674 | G | ALPHA-GALACTOSIDASE (EC 3.2.1.22) (MELIBIASE). |
| | ID0675 | G | XYLULOKINASE. |
| | ID0676 | G | 6-PHOSPHO-GLUCOSIDASE MALH. |
| 10 | ID0677 | G | PUTATIVE PTS SYSTEM IIBC COMPONENT YWBA (EC 2.7.1.69). |
| | ID0678 | G | HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION. |
| | ID0679 | G | YTCQ. |
| 15 | ID0680 | G | Bacillus subtilis araN gene product. |
| | ID0681 | G | ALTRONATE HYDROLASE (EC 4.2.1.7) (ALTRONIC ACID HYDRATASE). |
| | ID0682 | G | YBBT PROTEIN. |
| | ID0683 | G | YKRW PROTEIN. |
| 20 | ID0684 | G | CELLULASE. |
| | ID0685 | G | PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUC |
| | ID0686 | G | YESO PROTEIN. |
| | ID0687 | G | Amino acid sequence of tac promoter and Bacillus subtilis BR |
| 25 | ID0688 | G | RIBOSE TRANSPORT ATP-BINDING PROTEIN RBSA. |
| | ID0689 | G | PUTATIVE FAMILY 31 GLUCOSIDASE YICI. |
| | ID0690 | G | PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC ENZYME II, ABC COMP |
| 30 | ID0691 | G | GLUCONOKINASE (EC 2.7.1.12) (GLUCONATE KINASE). |
| | ID0692 | G | HYPOTHETICAL 34.0 KDA PROTEIN IN RHO-MURA INTERGENIC REGION |
| | ID0693 | G | YTOP. |
| | ID0694 | G | YTBD. |
| 35 | ID0695 | G | IOLH PROTEIN. |
| | ID0696 | G | 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE. |
| | ID0697 | G | 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1. |
| 40 | ID0698 | G | D-MANNONATE HYDROLASE. |
| | ID0699 | G | L-ARABINOSE MEMBRANE PERMEASE. |
| | ID0700 | G | HYPOTHETICAL 39.2 KDA PROTEIN. |
| | ID0701 | G | LPLB PROTEIN. |
| | ID0702 | G | SA2434 PROTEIN. |
| 45 | ID0703 | G | GLYCEROL-3-PHOSPHATE TRANSPORTER. |
| | ID0704 | G | MEMBRANE TRANSPORT PROTEIN. |
| | ID0705 | G | LIPOPROTEIN. |
| | ID0706 | G | GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (EC 2.7.7.27) (ADP-G |
| 50 | ID0707 | G | YJDE PROTEIN. |
| | ID0708 | G | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YESP. |
| | ID0709 | G | SUGAR-BINDING PROTEIN. |
| | ID0710 | G | HYPOTHETICAL 35.0 KDA PROTEIN. |
| | ID0711 | G | IOLE PROTEIN. |
| 55 | ID0712 | G | YBBF. |
| | ID0713 | G | PHOSPHOPENTOMUTASE (EC 5.4.2.7) (PHOSPHODEOXYRIBOMUTASE). |
| | ID0714 | G | LPLC PROTEIN. |
| | ID0715 | G | SUGAR ABC TRANSPORTOR (ATP-BINDING PROTEIN). |
| 60 | KINASE (EC | | BIFUNCTIONAL PGK/TIM [INCLUDES: PHOSPHOGLYCERATE |
| | ID0717 | G | PROBABLE 6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86). |
| | ID0718 | G | HYPOTHETICAL ALTRONATE OXIDOREDUCTASE. |
| | ID0719 | G | HYPOTHETICAL 30.9 KDA PROTEIN. |
| | ID0720 | G | IOLI PROTEIN. |
| 65 | ID0721 | G | TEICHOIC ACID TRANSLOCATION ATP-BINDING PROTEIN TAGH. |
| | ID0722 | G | D-MANNONATE DEHYDROLASE. |

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| | ID0723 | G | HYPOTHETICAL 45.5 KDA PROTEIN. |
| | ID0724 | G | ORF starting with ATG of length 2513 |
| | ID0725 | G | endo 1,5 alpha-L-arabinase |
| 5 | ID0726 | G | HYPOTHETICAL 31.3 KDA PROTEIN. |
| | ID0727 | G | ABC TRANSPORTER (PERMIASE). |
| | ID0728 | G | YKRP PROTEIN. |
| | ID0729 | G | 6-PHOSPHO-BETA-GLUCOSIDASE BGLB (EC 3.2.1.86). |
| | ID0730 | G | PROBABLE FRUCTOSE-BISPHTHOSPHATE ALDOLASE 2 (EC 4.1.2.13). |
| 10 | ID0731 | G | PROBABLE FRUCTOSE-BISPHTHOSPHATE ALDOLASE 1 (EC 4.1.2.13). |
| | ID0732 | G | SUGAR TRANSPORTER. |
| | ID0733 | G | PUTATIVE INTEGRAL PROTEIN. |
| 15 | ID0734 | G | SAC OPERON RELATED REGULATION PROTEIN (FRAGMENT). |
| | ID0735 | G | HYPOTHETICAL 59.0 KDA PROTEIN. |
| | ID0736 | G | D-RIBOSE-BINDING PROTEIN PRECURSOR. |
| | ID0737 | G | ALPHA-L-ARABINOFRANOSIDASE 1 (EC 3.2.1.55) (ARABINOSIDASE). |
| | ID0738 | G | YFHI. |
| 20 | ID0739 | G | PYRUVATE KINASE (EC 2.7.1.40) (PK). |
| | ID0740 | G | GLYCOGEN BIOSYNTHESIS PROTEIN GLGD. |
| | ID0741 | G | YUTF PROTEIN. |
| | ID0742 | G | 2-DEHYDRO-3-DEOXYGLUCONOKINASE (EC 2.7.1.45) (2-KETO-3-DEOXY |
| 25 | ID0743 | G | PUTATIVE CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE (EC |
| | ID0744 | G | PTS SYSTEM, GLUCOSE-SPECIFIC ENZYME II, A COMPONENT. |
| | ID0745 | G | YFJS PROTEIN. |
| 30 | ID0746 | G | PROBABLE D-GALACTARATE DEHYDRATASE (EC 4.2.1.42) (GALCD). |
| | ID0747 | G | RIBOKINASE (EC 2.7.1.15). |
| | ID0748 | G | HYPOTHETICAL 42.1 KDA PROTEIN. |
| | ID0749 | G | MANNITOL-1-PHOSPHATE 5-DEHYDROGENASE (EC 1.1.1.17). |
| 35 | ID0750 | G | HYPOTHETICAL 29.9 KDA PROTEIN IN SIGY-CYDD INTERGENIC REGION. |
| | ID0751 | G | HYPOTHETICAL 48.4 KDA PROTEIN. |
| | ID0752 | G | FRUCTOSE SPECIFIC PERMEASE. |
| | ID0753 | G | SUGAR TRANSPORTER. |
| 40 | ID0754 | G | HYPOTHETICAL 28.3 KDA PROTEIN IN KBA-A-FEUC INTERGENIC REGION. |
| | ID0755 | G | PHOSPHO-BETA-GLUCOSIDASE. |
| | ID0756 | G | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YESQ. |
| | ID0757 | G | GLYCOGEN SYNTHASE. |
| 45 | ID0758 | G | 6-PHOSPHO-BETA-GLUCOSIDASE A. |
| | ID0759 | G | B. licheniformis acid stable and thermostable alpha-amylase. |
| | ID0760 | G | PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC ENZYME II, |
| | ABC COMP | | |
| 50 | ID0761 | G | MULTIPLE SUGAR TRANSPORT SYSTEM (MULTIPLE SUGAR-BINDING PROT). |
| | ID0762 | G | SUCROSE-6-PHOSPHATE HYDROLASE E1 (EC 3.2.1.26) (SUCRASE E1). |
| | ID0763 | G | Bacillus sp. OC187 4(R)-hydroxy-2-ketoglutaric acid aldolase. |
| 55 | ID0764 | G | GALACTOKINASE (EC 2.7.1.6) (GALACTOSE KINASE). |
| | ID0765 | G | SUCRASE (EC 3.2.1.26). |
| | ID0766 | G | XYLAN BETA-1,4-XYLOSIDASE (EC 3.2.1.37). |
| | ID0767 | G | N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25). |
| 60 | ID0768 | G | GLUCONOKINASE (EC 2.7.1.12) (GLUCONATE KINASE). |
| | ID0769 | G | RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1) (PENTOSE-5-PHOSP). |
| | ID0770 | G | SUGAR KINASE. |
| | ID0771 | G | HOMOLOGOUS TO SWISSPROT:YADE_ECOLI. |
| 65 | ID0772 | G | PTS SYSTEM, ARBUTIN-LIKE IIBC COMPONENT (PHOSPHOTRANSFERASE). |

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| | ID0773 | G | SUGAR ABC TRANSPORTER (SUGAR-BINDING PROTEIN). |
| | ID0774 | G | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2 (EC |
| 1.2.1.12) (GA | | | |
| 5 | ID0775 | G | PUTATIVE SUGAR-TRANSPORT ATP BINDING PROTEIN. |
| | ID0776 | G | URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE |
| | ISOMERASE) (URO | | |
| | ID0777 | G | PUTATIVE PTS SYSTEM IIBC COMPONENT YWBA (EC |
| 2.7.1.69). | | | |
| 10 | ID0778 | G | URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE |
| | ISOMERASE) (URO | | |
| | ID0779 | G | 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC |
| 1.1.1. | | | |
| 15 | ID0780 | G | ORF starting with ATG of length 1998 |
| | ID0781 | G | HYPOTHETICAL 52.5 KDA PROTEIN IN HUTP-BGLP INTERGENIC |
| REGION | | | |
| | ID0782 | G | PROBABLE HEXULOSE-6-PHOSPHATE SYNTHASE (EC 4.1.2.-) |
| (HUMPS) | | | |
| | ID0783 | G | PROBABLE GALACTARATE TRANSPORTER (D-GALACTARATE |
| PERMEASE). | | | |
| 20 | ID0784 | G | TRANSALDOLASE (PENTOSE PHOSPHATE). |
| | ID0785 | G | 6-PHOSPHO-BETA-GLUCOSIDASE BGLA (EC 3.2.1.86). |
| | ID0786 | G | L-RIBULOSE-5-PHOSPHATE 4-EPIMERASE. |
| | ID0787 | G | KBAY. |
| | ID0788 | G | FRUCTOSE 1-PHOSPHATE KINASE. |
| 25 | ID0789 | G | YTEQ PROTEIN. |
| | ID0790 | G | BH0592 PROTEIN. |
| | ID0791 | G | HYPOTHETICAL 54.3 KDA PROTEIN. |
| | ID0792 | G | L-RIBULOSE-5-PHOSPHATE 4-EPIMERASE. |
| 30 | ID0793 | G | endo 1,5 alpha-L-arabinase |
| | ID0794 | G | CONSERVED HYPOTHETICAL PROTEIN, POSSIBLE |
| OXIDOREDUCTASE. | | | |
| | ID0795 | G | HYPOTHETICAL 21.3 KDA PROTEIN IN BLTR-SPOIIIC |
| INTERGENIC REG | | | |
| 35 | ID0796 | G | 358AA LONG HYPOTHETICAL TRANSPORTER ATP-BINDING |
| PROTEIN. | | | |
| | ID0797 | G | IOLC PROTEIN. |
| | ID0798 | G | PHOSPHOTRANSFERASE ENZYME II (EC 2.7.1.69) (PROTEIN- |
| N(PI)-PHO | | | |
| 40 | ID0799 | G | PTS SYSTEM ENZYME II ABC (ASC), CRYPTIC, TRANSPORTS |
| SPECIFIC | | | |
| | ID0800 | G | PTS SYSTEM, FRUCTOSE-SPECIFIC IIB COMPONENT (EIIB- |
| FRU) (FRUC | | | |
| | ID0801 | G | HYPOTHETICAL 22.0 KDA PROTEIN. |
| | ID0802 | G | N-ACETYLGLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC |
| 45 | 5.3.1.10). | | |
| | ID0803 | G | PUTATIVE XYLANASE (FRAGMENT). |
| | ID0804 | G | PUTATIVE ATP/GTP-BINDING PROTEIN. |
| | ID0805 | G | HYPOTHETICAL 37.2 KDA PROTEIN IN PBP-GGT INTERGENIC |
| REGION. | | | |
| 50 | ID0806 | G | D-XYLOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR. |
| | ID0807 | G | PEP-DEPENDENT PHOSPHOTRANSFERASE ENZYME II FOR |
| CELLOBIOSE. | | | |
| | ID0808 | G | ORF starting with ATG of length 1332 |
| | ID0809 | G | B.subtilis cysteine protease CP3 protein sequence. |
| 55 | ID0810 | G | HYPOTHETICAL LACA/RPIB FAMILY PROTEIN IN SPOIIR-GLYC |
| INTERGE | | | |
| | ID0811 | G | MALTOSE/MALTODEXTRIN-BINDING PROTEIN. |
| | ID0812 | G | ORF starting with ATG of length 1284 |
| | ID0813 | G | PUTATIVE PTS SYSTEM IIA COMPONENT YPQE (EC 2.7.1.69). |
| 60 | ID0814 | G | N-ACETYLGLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC |
| 5.3.1.10). | | | |
| | ID0815 | G | HYPOTHETICAL 48.4 KDA PROTEIN. |
| | ID0816 | G | KHG/KDPG ALDOLASE [INCLUDES: 4-HYDROXY-2-OXOGLUTARATE |
| ALDOLA | | | |
| 65 | ID0817 | G | PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT (EIIA- |
| FRU) (FRUC | | | |

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| | ID0818 | G | ABC TRANSPORTER SUGAR PERMEASE. |
| | ID0819 | G | NODB-LIKE PROTEIN. |
| | ID0820 | G | ORF starting with ATG of length 1098 |
| | ID0821 | G | 2-KETO-3-DEOXY-GLUCONATE KINASE. |
| 5 | ID0822 | G | ENZYME II SUCROSE PROTEIN (EC 2.7.1.69). |
| | ID0823 | G | AMYX PROTEIN. |
| | ID0824 | G | HYPOTHETICAL 79.2 KDA PROTEIN. |
| | ID0825 | G | HYPOTHETICAL 44.9 KDA PROTEIN. |
| | ID0826 | G | ABC TRANSPORTER SUGAR PERMEASE. |
| 10 | ID0827 | G | HYPOTHETICAL 31.7 KDA PROTEIN. |
| | ID0828 | G | ORF starting with ATG of length 993 |
| | ID0829 | G | ORF starting with ATG of length 975 |
| | ID0830 | G | HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YURM. |
| | ID0831 | G | TRANSKETOLASE. |
| 15 | ID0832 | G | PUTATIVE ABC TRANSPORTER, SUGAR PERMEASE PROTEIN. |
| | ID0833 | G | ORF starting with ATG of length 960 |
| | ID0834 | G | ENDO-1,4-BETA-XYLANASE. |
| | ID0835 | G | ORF starting with ATG of length 957 |
| 20 | ID0836 | G | ORF starting with ATG of length 936 |
| | ID0837 | G | ORF starting with ATG of length 1050 |
| | ID0838 | G | PTS SYSTEM ENZYME II ABC (ASC), CRYPTIC, TRANSPORTS |
| | SPECIFIC | | |
| | ID0839 | G | ORF starting with ATG of length 888 |
| | ID0840 | G | MALP. |
| 25 | ID0841 | G | SA1198 PROTEIN. |
| | ID0842 | G | AMYX PROTEIN. |
| | ID0843 | G | ORF starting with ATG of length 843 |
| | ID0844 | G | TRANSKETOLASE C-TERMINAL SECTION. |
| | ID0845 | G | Arabinose isomerase from <i>Bacillus licheniformis</i> , |
| 30 | deduced amo | | |
| | ID0846 | G | ORF starting with ATG of length 822 |
| | ID0847 | G | ORF starting with ATG of length 1231 |
| | ID0848 | G | ORF starting with ATG of length 816 |
| | ID0849 | G | BETA-GLUCOSIDE PERMEASE IIABC COMPONENT. |
| 35 | ID0850 | G | <i>Bacillus subtilis</i> L-arabinose isomerase. |
| | ID0851 | G | PUTATIVE TRANSALDOLASE. |
| | ID0852 | G | RHAMNOSE TRANSPORTER (FRAGMENT). |
| | ID0853 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA-CEL) (CE |
| 40 | ID0854 | G | MALTOSE/MALTODEXTRIN TRANSPORT SYSTEM |
| | (MALTOSE/MALTODEXTRIN-) | | |
| | ID0855 | G | ORF starting with ATG of length 1239 |
| | ID0856 | G | HPR PROTEIN. |
| | ID0857 | G | PTS SYSTEM, GLUCOSE-SPECIFIC ENZYME II, A COMPONENT. |
| 45 | ID0858 | G | ORF starting with ATG of length 705 |
| | ID0859 | G | PHOSPHOPENTOMUTASE (EC 5.4.2.7) |
| | (PHOSPHODEOXYRIBOMUTASE). | | |
| | ID0860 | G | ORF starting with ATG of length 687 |
| | ID0861 | G | FRUCTOSE 1-PHOSPHATE KINASE. |
| 50 | ID0862 | G | GLYCEROL-3-PHOSPHATE TRANSPORTER. |
| | ID0863 | G | PROBABLE PTS SYSTEM, TREHALOSE-SPECIFIC IIBC |
| | COMPONENT (EIIIB) | | |
| | ID0864 | G | PHOSPHOCARRIER PROTEIN HPR (CATABOLITE REPRESSION). |
| | ID0865 | G | ORF starting with ATG of length 576 |
| 55 | ID0866 | G | PUTATIVE MALTOSE PHOSPHORYLASE (EC 2.4.1.8) |
| | (FRAGMENT). | | |
| | ID0867 | G | HYPOTHETICAL 87.9 KDA PROTEIN. |
| | ID0868 | G | HYPOTHETICAL 38.4 KDA PROTEIN IN DPPE-HMP INTERGENIC |
| | REGION. | | |
| 60 | ID0869 | G | C4-DICARBOXYLATE TRANSPORT SYSTEM (C4-DICARBOXYLATE-BINDING) |
| | ID0870 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA-CEL) (CE |
| | ID0871 | G | METHYLGLYXAL SYNTHASE (EC 4.2.99.11) (MGS). |
| 65 | ID0872 | G | <i>S. pneumoniae</i> derived protein #352. |
| | ID0873 | G | ORF starting with ATG of length 516 |

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| | ID0874 | G | C4-DICARBOXYLATE TRANSPORT SYSTEM (C4-DICARBOXYLATE- |
| | BINDING | | |
| | ID0875 | G | SUCRASE-6-PHOSPHATE HYDROLASE. |
| | ID0876 | G | Enterococcus faecalis protein EF092. |
| 5 | ID0877 | G | SA0255 PROTEIN. |
| | ID0878 | G | Enterococcus faecalis protein EF092. |
| | ID0879 | G | S. pneumoniae cellobiose phosphotransferase system celA. |
| 10 | ID0880 | G | YTEP. |
| | ID0881 | G | GLYCEROL UPTAKE FACILITATOR PROTEIN. |
| | ID0882 | G | ORF starting with ATG of length 2513 |
| | ID0883 | G | ORF starting with ATG of length 429 |
| | ID0884 | G | ORF starting with ATG of length 402 |
| 15 | ID0885 | G | 6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE (EC 2.7.1.11) |
| | (PHOSPHOFRU | | |
| | ID0886 | G | ORF starting with ATG of length 351 |
| | ID0887 | G | MYO-INOSITOL CATABOLISM, IOLC. |
| | ID0888 | G | HYPOTHETICAL 35.3 KDA PROTEIN. |
| 20 | ID0889 | G | ORF starting with ATG of length 321 |
| | ID0890 | G | ORF starting with ATG of length 315 |
| | ID0891 | G | ORF starting with ATG of length 303 |
| | ID0892 | G | ORF starting with TTG or GTG of length 561 |
| | ID0893 | G | ORF starting with ATG of length 1368 |
| 25 | ID0894 | G | ORF starting with ATG of length 264 |
| | ID0895 | G | PHOSPHOTRANSFERASE EII (GLUCOSE) (FRAGMENT). |
| | ID0896 | G | PROBABLE D-GALACTARATE DEHYDRATASE (EC 4.2.1.42) |
| | (GALCD). | | |
| | ID0897 | GC | HYPOTHETICAL 43.0 KDA PROTEIN. |
| 30 | ID0898 | GC | HYPOTHETICAL GLYCOSYL TRANSFERASE. |
| | ID0899 | GC | HYPOTHETICAL 43.0 KDA PROTEIN. |
| | ID0900 | GC | HYPOTHETICAL GLYCOSYL TRANSFERASE. |
| | ID0901 | GE | GLUCONATE PERMEASE. |
| | ID0902 | GE | HYPOTHETICAL PROTEIN HI0092. |
| 35 | ID0903 | GEPR | HYPOTHETICAL 58.3 KDA PROTEIN IN GLPD-CSPB INTERGENIC REGION |
| | ID0904 | GEPR | MYO-INOSITOL TRANSPORT PROTEIN. |
| | ID0905 | GEPR | BICYCLOMYCIN RESISTANCE PROTEIN. |
| | ID0906 | GEPR | HYPOTHETICAL 48.7 KDA PROTEIN. |
| | ID0907 | GEPR | HYPOTHETICAL METABOLITE TRANSPORT PROTEIN IN GLVBC |
| 40 | 3'REGION. | | |
| | ID0908 | GEPR | YBFB PROTEIN. |
| | ID0909 | GEPR | BH2528 PROTEIN. |
| | ID0910 | GEPR | YFMO. |
| | ID0911 | GEPR | HOMOLOGUE OF MULTIDRUG RESISTANCE PROTEIN B, EMRB, OF E. COL |
| 45 | ID0912 | GEPR | MULTIDRUG TRANSPORTER. |
| | ID0913 | GEPR | HYPOTHETICAL 48.2 KDA PROTEIN IN COTF-TETB INTERGENIC REGION |
| | ID0914 | GEPR | HYPOTHETICAL. |
| 50 | ID0915 | GEPR | LMRB. |
| | ID0916 | GEPR | HYPOTHETICAL 52.7 KDA PROTEIN. |
| | ID0917 | GEPR | PROBABLE GALACTARATE TRANSPORTER (D-GALACTARATE PERMEASE). |
| | ID0918 | GEPR | MYO-INOSITOL TRANSPORT PROTEIN. |
| 55 | ID0919 | GEPR | MELY. |
| | ID0920 | GEPR | BENZOATE TRANSPORT PROTEIN. |
| | ID0921 | GEPR | YVMA. |
| | ID0922 | GEPR | HEXURONATE TRANSPORTER. |
| 60 | ID0923 | GEPR | HYPOTHETICAL 39.1 KDA PROTEIN IN KAPD-PBPD INTERGENIC REGION |
| | ID0924 | GEPR | ORF starting with ATG of length 1452 |
| | ID0925 | GEPR | YITG PROTEIN. |
| | ID0926 | GEPR | ORF starting with ATG of length 1434 |
| 65 | ID0927 | GEPR | HYPOTHETICAL 43.1 KDA PROTEIN. |
| | ID0928 | GEPR | HYPOTHETICAL 44.7 KDA PROTEIN IN GLNQ-ANSR INTERGENIC REGION |

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| | ID0929 | GEPR | ORF starting with ATG of length 1368 |
| | ID0930 | GEPR | MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX |
| | TRANSPORTER | | |
| 5 | ID0931 | GEPR | HYPOTHETICAL 44.7 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| | ID0932 | GEPR | ORF starting with ATG of length 1266 |
| | ID0933 | GEPR | ORF starting with ATG of length 1257 |
| | ID0934 | GEPR | LMRB. |
| 10 | ID0935 | GEPR | HEXURONATE TRANSPORTER. |
| | ID0936 | GEPR | ORF starting with ATG of length 1098 |
| | ID0937 | GEPR | ORF starting with ATG of length 1047 |
| | ID0938 | GEPR | ORF starting with ATG of length 993 |
| | ID0939 | GEPR | ORF starting with ATG of length 918 |
| 15 | ID0940 | GEPR | HYPOTHETICAL 44.2 KDA PROTEIN IN COTF-TETB INTERGENIC |
| | REGION | | |
| | ID0941 | GEPR | ORF starting with ATG of length 843 |
| | ID0942 | GEPR | YFKF PROTEIN. |
| | ID0943 | GEPR | ORF starting with ATG of length 747 |
| 20 | ID0944 | GEPR | PARTIAL PUTATIVE MEMBRANE TRANSPORT PROTEIN. |
| | ID0945 | GEPR | GLUCOSE TRANSPORTER 3. |
| | ID0946 | GEPR | SA2300 PROTEIN. |
| | ID0947 | GEPR | ORF starting with ATG of length 456 |
| | ID0948 | GEPR | SIMILAR TO METABOLITE TRANSPORT PROTEINS. |
| 25 | ID0949 | GEPR | BH0884 PROTEIN. |
| | ID0950 | GER | HYPOTHETICAL 37.8 KDA PROTEIN. |
| | ID0951 | GER | HYPOTHETICAL 33.8 KDA PROTEIN IN GLPT-PURT INTERGENIC |
| | REGION | | |
| | ID0952 | GER | HYPOTHETICAL 34.0 KDA PROTEIN IN GLTP-PCP INTERGENIC |
| 30 | REGION | | |
| | ID0953 | GER | BH1931 PROTEIN. |
| | ID0954 | GER | HYPOTHETICAL 30.5 KDA PROTEIN IN GDHI 5'REGION (ORF 2). |
| | ID0955 | GER | HYPOTHETICAL 33.0 KDA PROTEIN IN PELB-PENP INTERGENIC |
| 35 | REGION | | |
| | ID0956 | GER | BH2747 PROTEIN. |
| | ID0957 | GER | ORF starting with ATG of length 939 |
| | ID0958 | GER | ORF starting with ATG of length 912 |
| | ID0959 | GER | ORF starting with ATG of length 369 |
| 40 | ID0960 | GER | ORF starting with ATG of length 345 |
| | ID0961 | GR | YVRK PROTEIN. |
| | ID0962 | GR | YOAN. |
| | ID0963 | GT | YJDC PROTEIN. |
| | ID0964 | GT | PUTATIVE CEL OPERON REGULATOR. |
| 45 | ID0965 | GT | FRUCTOSE SPECIFIC PERMEASE (FRAGMENT). |
| | ID0966 | GT | BH0220 PROTEIN. |
| | ID0967 | GT | ORF starting with ATG of length 459 |
| | ID0968 | H | HYPOTHETICAL 53.0 KDA PROTEIN IN SFP-GERKA INTERGENIC |
| | REGION | | |
| | ID0969 | H | YUEK PROTEIN. |
| 50 | ID0970 | H | MENAQUINONE BIOSYNTHESIS PROTEIN MEND [INCLUDES: 2- |
| | SUCCINYL- | | |
| | ID0971 | H | THIAMINE BIOSYNTHESIS PROTEIN THIC. |
| | ID0972 | H | S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) |
| 55 | (METHIONINEADEN | | |
| | ID0973 | H | PROBABLE GLUCARATE DEHYDRATASE (EC 4.2.1.40) (GDH) |
| | (GLUCD) . | | |
| | ID0974 | H | GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-) (GLUTR). |
| | ID0975 | H | GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8) |
| | (GSA) (| | |
| 60 | ID0976 | H | B. subtilis rib operon protein translated from |
| | reading frame | | |
| | ID0977 | H | MOLYBDOPTERIN BIOSYNTHESIS PROTEIN. |
| | ID0978 | H | PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO). |
| | ID0979 | H | PROBABLE AMINOTRANSFERASE YODT (EC 2.6.---). |
| 65 | ID0980 | H | BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) . |

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| | ID0981 | H | 2-AMINO-3-KETOBUTYRATE COENZYME A LIGASE (EC |
| | 2.3.1.29) | (AKB | |
| | ID0982 | H | BH1152 PROTEIN. |
| | ID0983 | H | GLUTAMATE-1-SEMALDEHYDE 2,1-AMINOMUTASE 2 (EC |
| 5 | 5.4.3.8) | (GSA | |
| | ID0984 | H | YLOI PROTEIN. |
| | ID0985 | H | UROPORPHYRINOGENDECARBOXYLASE (EC 4.1.1.37) (URO-D) |
| | (UPD). | | |
| | ID0986 | H | YTFD. |
| 10 | ID0987 | H | PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III |
| | OXIDASE (E | | |
| | ID0988 | H | HYPOTHETICAL 38.0 KDA PROTEIN. |
| | ID0989 | H | QUINOLINATE SYNTHETASE. |
| 15 | ID0990 | H | FOLYL-POLYGLUTAMATE SYNTHASE (EC 6.3.2.17) (FOLYL-POLY- |
| | GAMMA-G | | |
| | ID0991 | H | MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN A (NARA |
| | PROTEIN). | | |
| | ID0992 | H | DIHYDROXYNAPHTHOATE SYNTHASE. |
| 20 | ID0993 | H | 8-AMINO-7-OXONONANOATE SYNTHASE (EC 2.3.1.47) (AONS) |
| | (8-AMIN | | |
| | ID0994 | H | MOLYBDOPTERIN BIOSYNTHESIS PROTEIN. |
| | ID0995 | H | YKFB. |
| | ID0996 | H | DENOXYL-METHIONINE-8-AMINO-7-OXONONANOATE |
| | AMINOTRANSFERASE. | | |
| 25 | ID0997 | H | YJBU PROTEIN. |
| | ID0998 | H | FOLD BIFUNCTIONAL PROTEIN [INCLUDES: |
| | METHYLENENETETRAHYDROFOLATE | | |
| | ID0999 | H | HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC |
| 30 | 2.5.1.30) | | |
| | ID1000 | H | PORPHOBILINOGENDEAMINASE (EC 4.3.1.8) (PBG) |
| | (HYDROXYMETHYLB | | |
| | ID1001 | H | <i>B. subtilis</i> pantothenate kinase, CoaA#1. |
| | ID1002 | H | DGOA PROTEIN [INCLUDES: 2-DEHYDRO-3- |
| | DEOXYPHOSPHOGALACTONATE | | |
| 35 | ID1003 | H | YITF PROTEIN. |
| | ID1004 | H | DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24) |
| | (PORPHOB | | |
| | ID1005 | H | NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1) (SPORE |
| | OUTGRO | | |
| 40 | ID1006 | H | 3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC |
| | 2.1.2.1 | | |
| | ID1007 | H | DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15) (DHPS) |
| | (DIHYDROPTEROA | | |
| | ID1008 | H | PROBABLE THIAMINE BIOSYNTHESIS PROTEIN THII. |
| 45 | ID1009 | H | SUPEROXIDE-INDUCIBLE PROTEIN. |
| | ID1010 | H | LYASE (NITROGEN-HYDROGEN) |
| | ID1011 | H | PUTATIVE S-ADENOSYL L-METHIONINE: UROPORPHYRINOGEN |
| | IIIMETHYL | | |
| | ID1012 | H | MENAQUINONE BIOSYNTHESIS METHYLTRANSFERASE (EC |
| 50 | 2.1.1.-) (SPO | | |
| | ID1013 | H | THIAMINE-MONOPHOSPHATE KINASE (EC 2.7.4.16) |
| | (THIAMINE-PHOSPH | | |
| | ID1014 | H | FERROCHELATASE. |
| | ID1015 | H | GERANYLTRANSTFERASE (EC 2.5.1.10) (FARNESYL- |
| 55 | DIPHOSPHATE | | |
| | ID1016 | H | RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBC [INCLUDES: |
| | RIBOFLAVIN K | | |
| | ID1017 | H | METHYLTRANSFERASE/UROPORPHYRINOGEN-III SYNTHASE. |
| | ID1018 | H | YJBV PROTEIN. |
| 60 | ID1019 | H | HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50) (4-METHYL- |
| | 5-BETA-H | | |
| | ID1020 | H | TRANSCRIPTIONAL REPRESSOR OF THE BIOTIN OPERON. |
| | ID1021 | H | HYPOTHETICAL 21.4 KDA PROTEIN IN DACA-SERS INTERGENIC |
| | REGION | | |
| 65 | ID1022 | H | DIPICOLINATE SYNTHASE, B CHAIN. |
| | ID1023 | H | HYPOTHETICAL 31.4 KDA PROTEIN IN PTA 3' REGION. |

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| | ID1024 | H | PROBABLE NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE |
| | [CARBOXYLAT | | |
| | ID1025 | H | Polypeptide encoded by rib operon of <i>Bacillus</i> |
| | subtilis. | | |
| 5 | ID1026 | H | HOMOLOGUE OF PHENYLACRYLIC ACID DECARBOXYLASE PAD1 OF YEAST. |
| | ID1027 | H | RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9). |
| | ID1028 | H | DETHILOBIOTIN SYNTHETASE (EC 6.3.3.3) (DETHILOBIOTIN SYNTHASE) |
| 10 | ID1029 | H | COMQ. |
| | ID1030 | H | UROPORPHYRINogen-III SYNTHASE (EC 4.2.1.75) (UROS) |
| | (UROPOREPH | | |
| | ID1031 | H | YLOS PROTEIN. |
| | ID1032 | H | THIAMIN BIOSYNTHESIS |
| 15 | ID1033 | H | BH2162 PROTEIN. |
| | ID1034 | H | PROBABLE NICOTINATE-NUCLEOTIDE ADENYLYLTRANSFERASE (EC 2.7.7) |
| | ID1035 | H | PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1) |
| | (PANTOTHENATE SYN | | |
| 20 | ID1036 | H | MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS |
| | PROTEIN B. | | |
| | ID1037 | H | DEPHOSPHO-COA KINASE (EC 2.7.1.24) (DEPHOSPHOCOENZYME A KINA |
| | ID1038 | H | MOLYBDOPTERIN CONVERTING FACTOR (SUBUNIT 2). |
| 25 | ID1039 | H | 6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9) |
| | (DMRL S | | |
| | ID1040 | H | Bradykinin gene product from plasmid pBLAK1. |
| | ID1041 | H | UNKNOWN (PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN). |
| | ID1042 | H | ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11) |
| 30 | (ASPARTATE | | |
| | ID1043 | H | PROBABLE 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (E |
| | ID1044 | H | ORF starting with ATG of length 984 |
| | ID1045 | H | 6-PYRUVOYL TETRAHYDROBIOPTERIN SYNTHASE HOMOLOGUE. |
| 35 | ID1046 | H | ASPARTATE OXIDASE (NADB) (EC 1.4.3.16). |
| | ID1047 | H | PROBABLE LIPOIC ACID SYNTHETASE (LIP-SYN) (LIPOATE SYNTHASE) |
| | ID1048 | H | DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25). |
| | ID1049 | H | LIPOIC ACID SYNTHASE. |
| 40 | ID1050 | H | ORF starting with ATG of length 675 |
| | ID1051 | H | 6-CARBOXYHEXANOATE--COA LIGASE (EC 6.2.1.14) |
| | (PIMELOYL-COASY | | |
| | ID1052 | H | 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE |
| 45 | ID1053 | H | Protein product of <i>Lactococcus lactis</i> DNA fragment. |
| | ID1054 | H | MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS |
| | PROTEIN A. | | |
| | ID1055 | H | PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN, PDXA. |
| | ID1056 | H | ORF starting with ATG of length 513 |
| 50 | ID1057 | H | YJBS PROTEIN. |
| | ID1058 | H | HYPOTHETICAL 21.4 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| | ID1059 | H | B. subtilis pantothenate synthetase. |
| | ID1060 | H | ORF starting with ATG of length 354 |
| 55 | ID1061 | H | Sirohem synthase protein. |
| | ID1062 | H | ORF starting with ATG of length 303 |
| | ID1063 | H | ORF starting with ATG of length 406 |
| | ID1064 | H | THIAMINE-MONOPHOSPHATE KINASE (EC 2.7.4.16) |
| | (THIAMINE-PHOSPH | | |
| 60 | ID1065 | HC | HYPOTHETICAL 54.4 KDA PROTEIN. |
| | ID1066 | HC | 4-HYDROXYBENZOATE 3-MONOXYGENASE (EC 1.14.13.2) (P- |
| | HYDROXYB | | |
| | ID1067 | HE | PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) |
| | (VEGETAT | | |
| 65 | ID1068 | HI | Synechocystis sp. 6803 DXP synthase protein sequence. |
| | ID1069 | HI | ORF starting with ATG of length 1536 |

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| | ID1070 | HI | Bacillus subtilis DXP synthase protein sequence. |
| | ID1071 | HI | Synechocystis sp. 6803 DXP synthase protein sequence. |
| | ID1072 | HQ | ISOCHORISMATE SYNTHASE DHBC (EC 5.4.99.6). |
| | ID1073 | HQ | MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6). |
| 5 | ID1074 | I | YUSL PROTEIN. |
| | ID1075 | I | YNGE PROTEIN. |
| | ID1076 | I | HYPOTHETICAL 72.2 KDA PROTEIN. |
| | ID1077 | I | YTCI. |
| 10 | ID1078 | I | PROBABLE CARDIOLIPIN SYNTHETASE 2 (EC 2.7.8.-) |
| | (CARDIOLIPIN | | |
| | ID1079 | I | SQUALENE-HOPENE CYCLASE. |
| | ID1080 | I | YUSK PROTEIN. |
| | ID1081 | I | YNGH. |
| 15 | ID1082 | I | BUTYRYL-COA DEHYDROGENASE. |
| | ID1083 | I | 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (EC 1.1.1.-) |
| | ID1084 | I | METHYLMALONYL-COA DECARBOXYLASE ALPHA SUBUNIT (EC 6.4.1.3). |
| 20 | ID1085 | I | ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT A |
| | ID1086 | I | MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) |
| | ID1087 | I | ACSA (FRAGMENT). |
| 25 | ID1088 | I | 4-DIPHOSPHOCYTIDYL-2-C-METHYL-D-ERYTHRITOL KINASE (EC 2.7.1. |
| | ID1089 | I | FATTY ACID/PHOSPHOLIPID SYNTHESIS PROTEIN PLSX. |
| | ID1090 | I | ACYL-COA DEHYDROGENASE (EC 1.3.99.). |
| | ID1091 | I | ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9). |
| 30 | ID1092 | I | ORF starting with ATG of length 1977 |
| | ID1093 | I | HYPOTHETICAL 45.8 KDA PROTEIN IN ACDA-NARI INTERGENIC REGION |
| | ID1094 | I | YVAB PROTEIN. |
| | ID1095 | I | YDBM PROTEIN. |
| 35 | ID1096 | I | 3-HYDROXYBUTYRYL-COA DEHYDROGENASE (EC 1.1.1.157). |
| | ID1097 | I | PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41) |
| | (CDP-DIGLYC | | |
| | ID1098 | I | FATTY ACID DESATURASE. |
| | ID1099 | I | UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) |
| 40 | (UPP SYN | | |
| | ID1100 | I | BUTYRATE ACETOACETATE-COA TRANSFERASE. |
| | ID1101 | I | ORF starting with ATG of length 1716 |
| | ID1102 | I | YUSJ PROTEIN. |
| | ID1103 | I | 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL SYNTHASE (EC 2.7.7 |
| 45 | ID1104 | I | FATTY ACID DESATURASE. |
| | ID1105 | I | PHAGE SHOCK PROTEIN A HOMOLOG. |
| | ID1106 | I | ACETYL-COA CARBOXYLASE BIOTIN CARBOXYLASE SUBUNIT (EC 6.4.1. |
| 50 | ID1107 | I | TYPE B CARBOXYLESTERASE (EC 3.1.1.1). |
| | ID1108 | I | PYRUVATE CARBOXYLASE (FRAGMENT). |
| | ID1109 | I | HYPOTHETICAL 30.7 KDA PROTEIN IN MCPC-KINA INTERGENIC REGION |
| | ID1110 | I | HYPOTHETICAL 19.9 KDA PROTEIN IN ILVD-THYB INTERGENIC REGION |
| 55 | ID1111 | I | HYPOTHETICAL 25.7 KDA PROTEIN IN GERAC-FHUC INTERGENIC REGION |
| | ID1112 | I | BUTYRYL-COA DEHYDROGENASE (EC 1.1.1.35) (3- |
| | HYDROXYACYL-COA DE | | |
| 60 | ID1113 | I | B. subtilis hydrolase protein YTPA. |
| | ID1114 | I | HYPOTHETICAL 18.7 KDA PROTEIN IN HOM-MRGA INTERGENIC REGION. |
| | ID1115 | I | CG5044 PROTEIN. |
| | ID1116 | I | SIMILAR TO HYDROXYMYRISTOYL- (ACYL CARRIER PROTEIN) |
| 65 | DEHYDRATA | | |

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| | ID1117 | I | PHOSPHATIDYL SERINE DECARBOXYLASE PROENZYME (EC 4.1.1.65). |
| | ID1118 | I | YHAR PROTEIN. |
| 5 | ID1119 | I | HYPOTHETICAL 35.4 KDA PROTEIN. |
| | ID1120 | I | ORF starting with ATG of length 1089 |
| | ID1121 | I | 3-HYDROXYBUTYRYL-COA DEHYDRATASE. |
| | ID1122 | I | BUTYRATE-ACETOACETATE COA-TRANSFERASE SUBUNIT B (EC 2.8.3.9) |
| 10 | ID1123 | I | 3-HYDROXYACYL-COA DEHYDROGENASE/ENOYL COA HYDRATASE (EC 1.1.1.1) |
| | ID1124 | I | 2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE SYNTHASE (MECP) |
| | ID1125 | I | ACETYL-COA SYNTHETASE (ACS-3). |
| 15 | ID1126 | I | TYPE B CARBOXYL ESTERASE (EC 3.1.1.1). |
| | ID1127 | I | CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3- |
| | PHOSPHATIDYL TRANS | | |
| | ID1128 | I | ORF starting with ATG of length 897 |
| | ID1129 | I | ORF starting with ATG of length 888 |
| 20 | ID1130 | I | ACETYL-COA CARBOXYLASE TRANSFERASE BETA SUBUNIT (EC 6.4.1.2) |
| | ID1131 | I | ORF starting with ATG of length 855 |
| | ID1132 | I | BH2687 PROTEIN. |
| | ID1133 | I | PUTATIVE ACYL-COA THIOESTER HYDROLASE YKHA (EC 3.1.2.-) |
| 25 | ID1134 | I | CFR-ASSOCIATED PROTEIN P70. |
| | ID1135 | I | ORF starting with ATG of length 630 |
| | ID1136 | I | ORF starting with ATG of length 627 |
| | ID1137 | I | BH1133 PROTEIN. |
| | ID1138 | I | YDBM PROTEIN. |
| 30 | ID1139 | I | HYPOTHETICAL 19.6 KDA PROTEIN IN SIPU-PBPC INTERGENIC REGION |
| | ID1140 | I | ORF starting with ATG of length 342 |
| | ID1141 | I | CG4784 PROTEIN. |
| | ID1142 | I | ACYL-COA DEHYDROGENASE (FRAGMENT). |
| 35 | ID1143 | I | MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) |
| | ID1144 | I | ACSA (FRAGMENT). |
| | ID1145 | IM | LYTB PROTEIN HOMOLOG. |
| 40 | ID1146 | IQ | YJAY PROTEIN. |
| | ID1147 | IQ | OSB-COA SYNTHASE. |
| | ID1148 | IQ | LONG-CHAIN-FATTY-ACID-COA LIGASE. |
| | ID1149 | IQ | LONG-CHAIN-FATTY-ACID--COA LIGASE (FADD-7). |
| | ID1150 | IQ | DNA encoding human synthetase #8. |
| 45 | ID1151 | IQ | ORF starting with ATG of length 1386 |
| | ID1152 | IQ | LONG-CHAIN-FATTY-ACID--COA LIGASE (FADD-7). |
| | ID1153 | IQ | D-ALANYL CARRIER PROTEIN (DCP). |
| | ID1154 | J | VALYL-TRNA SYNTHETASE (EC 6.1.1.9). |
| | ID1155 | J | THREONYL-TRNA SYNTHETASE 1 (EC 6.1.1.3) (THREONINE--TRNA LIG |
| 50 | ID1156 | J | ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIG |
| | ID1157 | J | TRANSLATIONAL ELONGATION FACTOR G. |
| | ID1158 | J | ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE |
| 55 | ID1159 | J | PHENYLALANYL-TRNA SYNTHETASE BETA SUBUNIT (EC 6.1.1.20) |
| | ID1160 | J | TRANSLATION INITIATION FACTOR IF-2. |
| | ID1161 | J | HYPOTHETICAL 58.2 KDA PROTEIN IN KLB-COTE INTERGENIC REGION. |
| 60 | ID1162 | J | PROLYL-TRNA SYNTHETASE. |
| | ID1163 | J | CYSTEINYLYL-TRNA SYNTHETASE (EC 6.1.1.16) (CYSTEINE--TRNA LIGA |
| | ID1164 | J | GLUTAMYL-TRNA (GLN) AMIDOTRANSFERASE SUBUNIT A. |
| | ID1165 | J | ASPARAGINYL-TRNA SYNTHETASE (EC 6.1.1.22) |
| 65 | (ASPARAGINE--TRNA | | |

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| | ID1166 | J | THREONYL-TRNA SYNTHETASE 2 (EC 6.1.1.3) (THREONINE-- |
| | TRNA LIG | | |
| | ID1167 | J | HYPOTHETICAL 51.7 KDA PROTEIN IN DNAJ-RPSU |
| | INTEREGENIC REGIO | | |
| 5 | ID1168 | J | SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA |
| | LIGASE) (S | | |
| | ID1169 | J | YFJO PROTEIN. |
| | ID1170 | J | GLYCYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.14) |
| | (GLYCINE--TR | | |
| 10 | ID1171 | J | TYROSYL-TRNA SYNTHETASE 1 (EC 6.1.1.1) (TYROSINE-- |
| | TRNA LIGAS | | |
| | ID1172 | J | HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-- |
| | TRNA LIGA | | |
| 15 | ID1173 | J | ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE--TRNA |
| | LIGASE) (| | |
| | ID1174 | J | TYROSYL-TRNA SYNTHETASE 2 (EC 6.1.1.1) (TYROSINE-- |
| | TRNA LIGAS | | |
| | ID1175 | J | PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)- |
| | METHYLTR | | |
| 20 | ID1176 | J | PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1). |
| | ID1177 | J | GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT B (EC |
| 6.3.5.-) (| | | |
| | ID1178 | J | GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-- |
| | TRNA LIGA | | |
| 25 | ID1179 | J | LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4). |
| | ID1180 | J | PUTATIVE TRANSLATION INITIATION FACTOR EIF-2B (EIF-2B |
| | GDP-GT | | |
| | ID1181 | J | LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA |
| | LIGASE) (LY | | |
| 30 | ID1182 | J | PROBABLE METHYLTRANSFERASE (EC 2.1.1.-). |
| | ID1183 | J | LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA |
| | LIGASE) (| | |
| | ID1184 | J | ATP PHOSPHORIBOSYLTRANSFERASE REGULATORY SUBUNIT. |
| | ID1185 | J | ELONGATION FACTOR TS (EF-TS). |
| 35 | ID1186 | J | TRYPTOPHANYL-TRNA SYNTHETASE (EC 6.1.1.2) |
| | (TRYPTOPHAN--TRNA | | |
| | ID1187 | J | POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC |
| 2.7.7.8) (POLY | | | |
| | ID1188 | J | POLY(A) POLYMERASE (EC 2.7.7.19) (PAP). |
| 40 | ID1189 | J | DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S- |
| | ADENOSYLMETHIO | | |
| | ID1190 | J | QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA- |
| | GUANINET | | |
| | ID1191 | J | 30S RIBOSOMAL PROTEIN S2 (BS1) (VEGETATIVE PROTEIN |
| 45 | 209) (VEG | | |
| | ID1192 | J | Streptococcus pneumoniae glycyl tRNA synthetase |
| | alpha. | | |
| | ID1193 | J | HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YACO (EC |
| | 2.1.1.-). | | |
| 50 | ID1194 | J | YFLG PROTEIN. |
| | ID1195 | J | METHIONINE AMINOPEPTIDASE (EC 3.4.11.18) (MAP). |
| | ID1196 | J | 30S RIBOSOMAL PROTEIN S3 (BS3) (BS2). |
| | ID1197 | J | RIBONUCLEASE PH (FRAGMENT). |
| | ID1198 | J | TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) |
| 55 | (PSEUDOURIDYLATE | | |
| | ID1199 | J | Aspartyl-tRNA synthetase from Staph. aureus. |
| | ID1200 | J | HYPOTHETICAL 29.7 KDA PROTEIN IN FOLD-AHRC INTERGENIC |
| | REGION | | |
| | ID1201 | J | HEMK PROTEIN HOMOLOG. |
| 60 | ID1202 | J | HYPOTHETICAL 33.7 KDA PROTEIN IN CSPB-GLPP INTERGENIC |
| | REGION | | |
| | ID1203 | J | HYPOTHETICAL P20 PROTEIN. |
| | ID1204 | J | TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA |
| | PSEUDOURID | | |
| 65 | ID1205 | J | HYPOTHETICAL 31.5 KDA PROTEIN IN MECA-TENA INTERGENIC |
| | REGION | | |

| | | | |
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| | ID1206 | J | PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) (PTH) (STAGE V |
| | SPORULA | | |
| | ID1207 | J | METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9). |
| | ID1208 | J | POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC |
| 5 | 2.7.7.8) (POLY | | |
| | ID1209 | J | HYPOTHETICAL 37.0 KDA PROTEIN IN SPOIIR-GLYC |
| | INTERGENIC REGI | | |
| | ID1210 | J | Methionyl-tRNA synthetase from Staph. aureus. |
| | ID1211 | J | POLYPEPTIDE DEFORMYLASE 2 (EC 3.5.1.31) (PDF 2) |
| 10 | (FORMYLMETHI | | |
| | ID1212 | J | HYPOTHETICAL 22.0 KDA PROTEIN IN FLIT-SECA INTERGENIC |
| | REGION | | |
| | ID1213 | J | 30S RIBOSOMAL PROTEIN S7 (BS7). |
| | ID1214 | J | HYPOTHETICAL 22.5 KDA PROTEIN IN RPLL-RPOB INTERGENIC |
| 15 | REGION | | |
| | ID1215 | J | PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN (EC |
| | 6.1.1.20) (PHEN | | |
| | ID1216 | J | 50S RIBOSOMAL PROTEIN L10 (BL5) (COLD ACCLIMATIZATION |
| | PROTEI | | |
| 20 | ID1217 | J | ORF starting with ATG of length 1479 |
| | ID1218 | J | 50S RIBOSOMAL PROTEIN L3 (BL3). |
| | ID1219 | J | 50S RIBOSOMAL PROTEIN L13. |
| | ID1220 | J | 50S RIBOSOMAL PROTEIN L16. |
| | ID1221 | J | 50S RIBOSOMAL PROTEIN L15. |
| 25 | ID1222 | J | S-ADENOSYLMETHIONINE:TRNA RIBOSYLTRANSFERASE- |
| | ISOMERASE (EC 5 | | |
| | ID1223 | J | YJCG PROTEIN. |
| | ID1224 | J | ERM2 PROTEIN. |
| | ID1225 | J | 16S PSEUDOURIDYLATE SYNTHASE. |
| 30 | ID1226 | J | 30S RIBOSOMAL PROTEIN S11 (BS11). |
| | ID1227 | J | 30S RIBOSOMAL PROTEIN S9 (BS10). |
| | ID1228 | J | GLYCYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.14) |
| | (GLYCINE--TR | | |
| | ID1229 | J | PUTATIVE REGULATOR OF PURINE BIOSYNTHESIS. |
| 35 | ID1230 | J | S-ADENOSYLMETHIONINE TRNA RIBOSYLTRANSFERASE. |
| | ID1231 | J | RRNA METHYLASE HOMOLOG. |
| | ID1232 | J | AT1G08980/F7G19_15. |
| | ID1233 | J | 30S RIBOSOMAL PROTEIN S13. |
| | ID1234 | J | 50S RIBOSOMAL PROTEIN L14. |
| 40 | ID1235 | J | GENERAL STRESS PROTEIN CTC. |
| | ID1236 | J | RIBOSOME-BINDING FACTOR A (P15B PROTEIN). |
| | ID1237 | J | 50S RIBOSOMAL PROTEIN L17. |
| | ID1238 | J | ELONGATION FACTOR P (EF-P). |
| | ID1239 | J | 50S RIBOSOMAL PROTEIN L6 (BL10). |
| 45 | ID1240 | J | 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE. |
| | ID1241 | J | 50S RIBOSOMAL PROTEIN L24 (BL23) (12 KDA DNA-BINDING |
| | PROTEIN | | |
| | ID1242 | J | ORF starting with ATG of length 989 |
| | ID1243 | J | ORF starting with ATG of length 964 |
| 50 | ID1244 | J | SA0330 PROTEIN. |
| | ID1245 | J | BH1243 PROTEIN. |
| | ID1246 | J | 30S RIBOSOMAL PROTEIN S19 (BS19). |
| | ID1247 | J | HYPOTHETICAL 37.0 KDA PROTEIN IN SPOIIR-GLYC |
| | INTERGENIC REGI | | |
| 55 | ID1248 | J | 30S RIBOSOMAL PROTEIN S1 HOMOLOG. |
| | ID1249 | J | ORF starting with ATG of length 873 |
| | ID1250 | J | HYPOTHETICAL 18.7 KDA PROTEIN. |
| | ID1251 | J | Glutamyl-tRNA(Gln) amidotransferase subunit ratc |
| | subunit. | | |
| 60 | ID1252 | J | 30S RIBOSOMAL PROTEIN S17 (BS16). |
| | ID1253 | J | 50S RIBOSOMAL PROTEIN L27 (BL30) (BL24). |
| | ID1254 | J | 30S RIBOSOMAL PROTEIN S8 (BS8). |
| | ID1255 | J | 50S RIBOSOMAL PROTEIN L20. |
| 65 | ID1256 | J | RHIZOBACTIN SIDEROPHORE BIOSYNTHESIS PROTEIN RHSD. |
| | ID1257 | J | ALANYL-TRNA SYNTHETASE (ALAS). |
| | ID1258 | J | 30S RIBOSOMAL PROTEIN S18 (BS21). |

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| | ID1259 | J | A formate transport associated protein, FMD. |
| | ID1260 | J | HYPOTHETICAL 9.7 KDA PROTEIN IN MFD-DIVIC INTERGENIC |
| | REGION | | |
| 5 | ID1261 | J | HYPOTHETICAL 21.1 KDA PROTEIN IN AMYX-OPUD INTERGENIC |
| | REGION | | |
| | ID1262 | J | TRANSLATION INITIATION FACTOR IF-1. |
| | ID1263 | J | 30S RIBOSOMAL PROTEIN S20 (BS20). |
| | ID1264 | J | YJCK PROTEIN. |
| 10 | ID1265 | J | ORF starting with ATG of length 705 |
| | ID1266 | J | BH1498 PROTEIN. |
| | ID1267 | J | PHE-TRNA SYNTHETASE ALPHA CHAIN. |
| | ID1268 | J | SPERMIDINE N1-ACETYLTRANSFERASE (EC 2.3.1.57) |
| | (DIAMINEACETYL | | |
| 15 | ID1269 | J | CG8684 PROTEIN. |
| | ID1270 | J | 30S RIBOSOMAL PROTEIN S6 (BS9). |
| | ID1271 | J | TRNA-GUANINE TRANSGLYCOSYLASE. |
| | ID1272 | J | ORF starting with ATG of length 600 |
| | ID1273 | J | 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE. |
| 20 | ID1274 | J | HYPOTHETICAL 12.3 KDA PROTEIN IN RPLU-RPMA INTERGENIC |
| | REGION | | |
| | ID1275 | J | 50S RIBOSOMAL PROTEIN L5 (BL6). |
| | ID1276 | J | YFKH PROTEIN. |
| | ID1277 | J | 50S RIBOSOMAL PROTEIN L30 (BL27). |
| | ID1278 | J | SA1699 PROTEIN. |
| 25 | ID1279 | J | ORF starting with ATG of length 537 |
| | ID1280 | J | ORF starting with ATG of length 510 |
| | ID1281 | J | ORF starting with ATG of length 507 |
| | ID1282 | J | TRANSLATION INITIATION FACTOR IF-3. |
| 30 | ID1283 | J | 50S RIBOSOMAL PROTEIN L7/L12 (BL9) ('A' TYPE) |
| | (VEGETATIVE PR | | |
| | ID1284 | J | RIBOSOMAL PROTEIN S15 (BS18). |
| | ID1285 | J | 50S RIBOSOMAL PROTEIN L2 (BL2). |
| | ID1286 | J | SPERMIDINE N1-ACETYLTRANSFERASE (EC 2.3.1.57) |
| | (DIAMINEACETYL | | |
| 35 | ID1287 | J | ORF starting with ATG of length 477 |
| | ID1288 | J | TRANSLATION INITIATION INHIBITOR, PUTATIVE. |
| | ID1289 | J | 50S RIBOSOMAL PROTEIN L22. |
| | ID1290 | J | PROTEIN SYNTHESIS INHIBITOR, PUTATIVE. |
| | ID1291 | J | ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-- |
| 40 | TRNA LIGA | | |
| | ID1292 | J | BH0940 PROTEIN. |
| | ID1293 | J | 50S RIBOSOMAL PROTEIN L28. |
| | ID1294 | J | 50S RIBOSOMAL PROTEIN L22. |
| | ID1295 | J | ELONGATION FACTOR-P HOMOLOG (FRAGMENT). |
| 45 | ID1296 | J | THREONYL-TRNA SYNTHETASE 1 (EC 6.1.1.3) (THREONINE-- |
| | TRNA LIG | | |
| | ID1297 | J | HYPOTHETICAL 29.7 KDA PROTEIN IN FOLD-AHRC INTERGENIC |
| | REGION | | |
| | ID1298 | J | PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) (FRAGMENT). |
| 50 | ID1299 | J | GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17). |
| | ID1300 | J | ORF starting with ATG of length 318 |
| | ID1301 | J | GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-- |
| | TRNA LI | | |
| | ID1302 | J | ORF starting with ATG of length 270 |
| 55 | ID1303 | J | ORF starting with TTG or GTG of length 497 |
| | ID1304 | J | ORF starting with ATG of length 228 |
| | ID1305 | J | ORF starting with ATG of length 225 |
| | ID1306 | J | ORF starting with TTG or GTG of length 438 |
| | ID1307 | J | HYPOTHETICAL 18.7 KDA PROTEIN. |
| 60 | ID1308 | J | RIBONUCLEASE PH (FRAGMENT). |
| | ID1309 | JE | ELONGATION FACTOR TU (EF-TU) (P-40). |
| | ID1310 | K | DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) |
| | (TRANSCR | | |
| 65 | ID1311 | K | DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2.7.7.6) |
| | (TRANS | | |
| | ID1312 | K | YTDP PROTEIN. |

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| | ID1313 | K | RNA POLYMERASE SIGMA FACTOR RPOD (SIGMA-A) (SIGMA-43). |
| | ID1314 | K | N UTILIZATION SUBSTANCE PROTEIN A HOMOLOG. |
| 5 | ID1315 (TRANSC | K | DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN (EC 2.7.7.6) |
| | ID1316 | K | TRANSCRIPTION TERMINATION FACTOR RHO. |
| | ID1317 | K | CENTRAL GLYCOLYTIC GENES REGULATOR. |
| | ID1318 | K | HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA. |
| 10 | ID1319 | K | DEOXYRIBONUCLEOSIDE REGULATOR. |
| | ID1320 | K | VIRULENCE-ASSOCIATED PROTEIN. |
| | ID1321 INTERGENI | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN CLPP-CRH |
| | ID1322 | K | SIGMA-B GENERAL STRESS TRANSCRIPTION FACTOR. |
| 15 | ID1323 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YKUM. |
| | ID1324 | K | TRANSCRIPTIONAL REGULATORY PROTEIN GLTC. |
| | ID1325 | K | RNA POLYMERASE SIGMA-54 FACTOR. |
| | ID1326 gene co | K | B. subtilis novel pantothenate kinase encoded by the |
| | ID1327 | K | STAGE 0 SPORULATION PROTEIN J. |
| 20 | ID1328 REGULATOR. | K | PROBABLE HTH_ARAC_FAMILY OF TRANSCRIPTIONAL |
| | ID1329 (P31) (ST | K | RNA POLYMERASE SIGMA-E FACTOR PRECURSOR (SIGMA-29) |
| 25 | ID1330 | K | YKVZ PROTEIN. |
| | ID1331 | K | PUTATIVE FIBRONECTIN-BINDING PROTEIN (YLOA PROTEIN). |
| | ID1332 | K | YKOZ PROTEIN. |
| | ID1333 | K | XYL REPRESSOR. |
| | ID1334 | K | LACI REPRESSOR-LIKE PROTEIN (YJMH PROTEIN). |
| 30 | ID1335 | K | RNA POLYMERASE SIGMA-28 FACTOR PRECURSOR. |
| | ID1336 | K | PUTATIVE FIBRONECTIN-BINDING PROTEIN (YLOA PROTEIN). |
| | ID1337 SUBTIL | K | HOMOLOGUE OF ALS OPERON REGULATORY PROTEIN ALSR OF B. |
| | ID1338 | K | ALS OPERON REGULATORY PROTEIN. |
| 35 | ID1339 PROTEIN | K | RNA POLYMERASE SIGMA-G FACTOR (STAGE III SPORULATION |
| | ID1340 | K | HYPOTHETICAL 37.7 KDA PROTEIN. |
| | ID1341 | K | KDG OPERON REPRESSOR. |
| | ID1342 | K | TRANSCRIPTIONAL ACTIVATOR TENA. |
| 40 | ID1343 INTERGEN | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GLTP-CWLJ |
| | ID1344 PGSA INTER | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOIIIE- |
| | ID1345 | K | LACI-FAMILY TRANSCRIPTION REGULATOR. |
| 45 | ID1346 AMYLASE REG | K | RNA POLYMERASE SIGMA-H FACTOR (SIGMA-30). |
| | ID1347 | K | CATABOLITE CONTROL PROTEIN A (GLUCOSE-RESISTANCE |
| | ID1348 REGION | K | HYPOTHETICAL 33.3 KDA PROTEIN IN FEUA-SIGW INTERGENIC |
| | ID1349 | K | PUTATIVE FRUCTOKINASE (EC 2.7.1.4). |
| 50 | ID1350 | K | RNA POLYMERASE SIGMA-D FACTOR (SIGMA-28). |
| | ID1351 | K | TREHALOSE OPERON TRANSCRIPTIONAL REPRESSOR. |
| | ID1352 INTERGEN | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SIPU-PBPC |
| | ID1353 REGION | K | HYPOTHETICAL 29.3 KDA PROTEIN IN GLVA-GLVC INTERGENIC |
| | ID1354 | K | RNA POLYMERASE SIGMA FACTOR SIGW. |
| | ID1355 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YWFK. |
| | ID1356 TRANSPORTER GE | K | TRANSCRIPTIONAL ACTIVATOR OF MULTIDRUG-EFFLUX |
| 60 | ID1357 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YWBI. |
| | ID1358 INTERGEN | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN MRGA-CITG |
| | ID1359 | K | PROTEASE PRODUCTION REGULATORY PROTEIN HPR. |
| | ID1360 | K | TRANSCRIPTIONAL REPRESSOR OF THE XYLOSE OPERON. |
| 65 | ID1361 | K | STAGE V SPORULATION PROTEIN T. |
| | ID1362 | K | HYPOTHETICAL 24.3 KDA PROTEIN (YVFI PROTEIN). |

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| | ID1363 | K | YDHQ PROTEIN. |
| | ID1364 | K | Gene product which inhibits production of coenzymes |
| | and intr | | |
| 5 | ID1365 | K | RNA POLYMERASE SIGMA FACTOR SIGX. |
| | ID1366 | K | YUGG PROTEIN. |
| | ID1367 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN HEMY-GLTT |
| | INTERGEN | | |
| | ID1368 | K | YEEK PROTEIN. |
| | ID1369 | K | BH0411 PROTEIN. |
| 10 | ID1370 | K | HYPOTHETICAL PROTEIN YWRC. |
| | ID1371 | K | TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT |
| | CLEAVAGE FA | | |
| | ID1372 | K | MEMBRANE-BOUND PROTEIN LYTR. |
| | ID1373 | K | HYPOTHETICAL 21.1 KDA PROTEIN IN GBSA-TLBB INTERGENIC |
| 15 | REGION | | |
| | ID1374 | K | TRANSCRIPTIONAL REGULATOR (MARR FAMILY). |
| | ID1375 | K | PEPTIDE METHIONINE SULFOXIDE REDUCTASE REGULATOR. |
| | ID1376 | K | BH0391 PROTEIN. |
| 20 | ID1377 | K | HYPOTHETICAL 21.3 KDA PROTEIN (ORF-1). |
| | ID1378 | K | Modified penicillinase repressor penI gene product. |
| | ID1379 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN WPRA-DEGA |
| | INTERGEN | | |
| | ID1380 | K | RNA POLYMERASE SIGMA FACTOR SIGY. |
| | ID1381 | K | TRANSCRIPTIONAL REGULATOR LRPC. |
| 25 | ID1382 | K | ATTENUATOR FOR LYTABC AND LYTR EXPRESSION. |
| | ID1383 | K | SIMILAR TO B. SUBTILIS YWGB GENE (BH0656 PROTEIN). |
| | ID1384 | K | YKVE PROTEIN. |
| | ID1385 | K | YWQ [A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] GENES. |
| 30 | ID1386 | K | PUTATIVE RNA POLYMERASE SIGMA FACTOR YLAC. |
| | ID1387 | K | YFMP. |
| | ID1388 | K | GLUCONATE OPERON TRANSCRIPTIONAL REPRESSOR. |
| | ID1389 | K | HYPOTHETICAL 16.6 KDA PROTEIN IN GLPD-SPOVR |
| | INTERGENIC REGIO | | |
| | ID1390 | K | HYPOTHETICAL 20.7 KDA PROTEIN IN BLTR-SPOIIC |
| 35 | INTERGENIC REG | | |
| | ID1391 | K | SINR PROTEIN. |
| | ID1392 | K | HYPOTHETICAL 14.5 KDA PROTEIN IN GAPB-MUTM INTERGENIC |
| | REGION | | |
| | ID1393 | K | REGULATORY PROTEIN. |
| 40 | ID1394 | K | RNA POLYMERASE ECF-TYPE SIGMA FACTOR. |
| | ID1395 | K | RIBONUCLEASE R (EC 3.1.---) (RNASE R) (VACB PROTEIN |
| | HOMOLOG) | | |
| | ID1396 | K | ORF starting with ATG of length 1056 |
| | ID1397 | K | RIBOSE OPERON REPRESSOR. |
| 45 | ID1398 | K | N UTILIZATION SUBSTANCE PROTEIN B HOMOLOG (NUSB |
| | PROTEIN). | | |
| | ID1399 | K | ORF starting with ATG of length 1047 |
| | ID1400 | K | HYPOTHETICAL 17.6 KDA PROTEIN. |
| | ID1401 | K | YRHO. |
| 50 | ID1402 | K | SCGR GENE. |
| | ID1403 | K | BH3951 PROTEIN. |
| | ID1404 | K | RIBONUCLEASE III (EC 3.1.26.3) (RNASE III). |
| | ID1405 | K | TRANSCRIPTIONAL REGULATOR LRPA. |
| | ID1406 | K | HYPOTHETICAL 14.7 KDA PROTEIN. |
| 55 | ID1407 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YTLL. |
| | ID1408 | K | HYPOTHETICAL 32.8 KDA PROTEIN IN SPOOJ-GIDB |
| | INTERGENIC REGIO | | |
| | ID1409 | K | HYPOTHETICAL 15.9 KDA PROTEIN. |
| | ID1410 | K | YKOM.. |
| 60 | ID1411 | K | YKMA. |
| | ID1412 | K | 30S RIBOSOMAL PROTEIN S21. |
| | ID1413 | K | DNA-DIRECTED RNA POLYMERASE DELTA SUBUNIT (RNAP DELTA |
| | FACTOR | | |
| | ID1414 | K | BH1561 PROTEIN. |
| 65 | ID1415 | K | BH0575 PROTEIN. |
| | ID1416 | K | BH1889 PROTEIN. |

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| | ID1417 | K | TRANSCRIPTIONAL REGULATOR (ICLR FAMILY). |
| | ID1418 | K | ORF starting with ATG of length 882 |
| | ID1419 | K | YOZA PROTEIN. |
| 5 | ID1420 | K | ORF starting with ATG of length 879 |
| | ID1421 | K | HYPOTHETICAL 12.8 KDA PROTEIN IN ODHA-CTPA INTERGENIC REGION |
| | ID1422 | K | ORF starting with ATG of length 858 |
| | ID1423 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GNTR-HTPG INTERGEN |
| 10 | ID1424 | K | ORF starting with ATG of length 855 |
| | ID1425 | K | PUTATIVE TRANSITION STATE REGULATOR ABH. |
| | ID1426 | K | ORF starting with ATG of length 837 |
| | ID1427 | K | TRANSCRIPTIONAL REPRESSOR (BETA-GALACTOSIDASE GENE). |
| 15 | ID1428 | K | ORF starting with ATG of length 813 |
| | ID1429 | K | ORF starting with ATG of length 804 |
| | ID1430 | K | BH0353 PROTEIN. |
| | ID1431 | K | VIRULENCE-ASSOCIATED PROTEIN. |
| | ID1432 | K | YVNA. |
| | ID1433 | K | BH2909 PROTEIN. |
| 20 | ID1434 | K | ORF starting with ATG of length 741 |
| | ID1435 | K | RNA POLYMERASE SPORULATION FORESPORE-SPECIFIC (LATE) SIGMA-G |
| | ID1436 | K | HYPOTHETICAL 21.1 KDA PROTEIN IN TDK-PRFA INTERGENIC REGION. |
| 25 | ID1437 | K | ORF starting with ATG of length 729 |
| | ID1438 | K | PUTATIVE GNTR-FAMILY REGULATORY PROTEIN. |
| | ID1439 | K | SORBITOL OPERON REGULATOR (SOR OPERON ACTIVATOR). |
| | ID1440 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN DINB-PHOB INTERGEN |
| 30 | ID1441 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1442 | K | TRANSCRIPTIONAL REPRESSOR (BETA-GALACTOSIDASE GENE). |
| | ID1443 | K | TRANSCRIPTIONAL REPRESSOR OF THE RIBOSE OPERON. |
| | ID1444 | K | HYPOTHETICAL 14.1 KDA PROTEIN IN TLPC-SRFAA |
| 35 | ID1445 | K | HYPOTHETICAL 8.2 KDA PROTEIN IN BLTR-SPOIIC INTERGENIC REGION |
| | ID1446 | K | ARAR. |
| | ID1447 | K | ORF starting with ATG of length 624 |
| | ID1448 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOIIC-CWLA INTER |
| 40 | ID1449 | K | ORF starting with ATG of length 615 |
| | ID1450 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UVRX-ILVA INTERGEN |
| | ID1451 | K | ORF starting with ATG of length 606 |
| 45 | ID1452 | K | HYPOTHETICAL 14.5 KDA PROTEIN. |
| | ID1453 | K | ORF starting with ATG of length 600 |
| | ID1454 | K | ORF starting with ATG of length 597 |
| | ID1455 | K | ORF starting with ATG of length 585 |
| | ID1456 | K | YDET PROTEIN. |
| 50 | ID1457 | K | YVBA PROTEIN. |
| | ID1458 | K | ORF starting with ATG of length 573 |
| | ID1459 | K | TRANSCRIPTIONAL REGULATOR OF EXTRACELLULAR ENZYME GENES. |
| | ID1460 | K | PUTATIVE TETR FAMILY TRANSCRIPTIONAL REGULATOR. |
| 55 | ID1461 | K | YLOH PROTEIN. |
| | ID1462 | K | BH0406 PROTEIN. |
| | ID1463 | K | Barstar protein sequence. |
| | ID1464 | K | BH0521 PROTEIN. |
| 60 | ID1465 | K | ORF starting with ATG of length 519 |
| | ID1466 | K | RNA POLYMERASE SIGMA-G FACTOR (STAGE III SPORULATION PROTEIN) |
| | ID1467 | K | RNA POLYMERASE SIGMA FACTOR SIGV. |
| | ID1468 | K | HYPOTHETICAL 14.5 KDA PROTEIN. |
| | ID1469 | K | MERCURIC RESISTANCE OPERON REGULATORY PROTEIN. |
| 65 | ID1470 | K | RPOC PROTEIN (DNA-DIRECTED RNA POLYMERASE BETA SUBUNIT) (EC |

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| | ID1471 | K | ACTIVATOR PROTEIN.. |
| | ID1472 | K | ORF starting with ATG of length 477 |
| | ID1473 | K | AUTOLYSIN ATLE AND PUTATIVE TRANSCRIPTIONAL REGULATOR |
| | ATLR G | | |
| 5 | ID1474 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN LYSP-NFO |
| | INTERGENI | | |
| | ID1475 | K | ORF starting with ATG of length 783 |
| | ID1476 | K | TRANSCRIPTIONAL REGULATOR (ARAC/XYLS FAMILY). |
| | ID1477 | K | ORF starting with ATG of length 396 |
| 10 | ID1478 | K | ORF starting with ATG of length 387 |
| | ID1479 | K | BH3535 PROTEIN. |
| | ID1480 | K | HYPOTHETICAL PROTEIN MTH1285. |
| | ID1481 | K | HYPOTHETICAL 14.5 KDA PROTEIN. |
| | ID1482 | K | RRF2 PROTEIN. |
| 15 | ID1483 | K | MLR8761 PROTEIN. |
| | ID1484 | K | HYPOTHETICAL 46.4 KDA PROTEIN. |
| | ID1485 | K | Y0ZG PROTEIN. |
| | ID1486 | K | YORF [A,B,C,D,E] , FTSL, PBPX AND REGR GENES. |
| | ID1487 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR MJ0272. |
| 20 | ID1488 | K | ORF starting with ATG of length 342 |
| | ID1489 | K | PUTATIVE TRANSCRIPTIONAL REGULATOR OF SORBOSE UPTAKE |
| | AND UTI | | |
| | ID1490 | K | ORF starting with ATG of length 315 |
| | ID1491 | K | SINR PROTEIN. |
| 25 | ID1492 | K | PROBABLE GNTR-FAMILY REGULATOR. |
| | ID1493 | K | YTCG (DNAB) . |
| | ID1494 | K | RNA POLYMERASE SIGMA FACTOR SIGK. |
| | ID1495 | K | ORF starting with ATG of length 255 |
| | ID1496 | K | ORF starting with ATG of length 225 |
| 30 | ID1497 | K | SIGMA-B GENERAL STRESS TRANSCRIPTION FACTOR. |
| | ID1498 | KE | HYPOTHETICAL 50.8 KDA PROTEIN IN SRFA4-SFP INTERGENIC |
| | REGION | | |
| | ID1499 | KE | YDEL PROTEIN. |
| | ID1500 | KE | HOMOLOGUE OF REGULATORY PROTEIN MOCR OF R. MELILOTI. |
| 35 | ID1501 | KE | YDEL PROTEIN. |
| | ID1502 | KE | HYPOTHETICAL 48.9 KDA PROTEIN PH0207. |
| | ID1503 | KG | DNA-BINDING PROTEIN IOLR. |
| | ID1504 | KG | SIMILAR TO PHOSPHOTRANSFERASE SYSTEM REGULATOR. |
| | ID1505 | KG | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA |
| 40 | REGION, | | |
| | ID1506 | KG | YTZE PROTEIN. |
| | ID1507 | KG | TRANSCRIPTIONAL REGULATOR (DEOR FAMILY) . |
| | ID1508 | KL | YWQA PROTEIN (MEMBER OF THE SNF2 HELICASE FAMILY). |
| | ID1509 | KL | HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION. |
| 45 | ID1510 | KL | YWQA PROTEIN (MEMBER OF THE SNF2 HELICASE FAMILY) . |
| | ID1511 | KN | NEGATIVE REGULATOR OF FLAGELLIN SYNTHESIS (ANTI- |
| | SIGMA-D FACT | | |
| | ID1512 | KR | YBFA PROTEIN. |
| | ID1513 | KR | PROTEASE SYNTHASE AND SPORULATION NEGATIVE REGULATORY |
| 50 | PROTEI | | |
| | ID1514 | KR | CGEE PROTEIN. |
| | ID1515 | KR | YJCF PROTEIN. |
| | ID1516 | KR | BH2157 PROTEIN. |
| | ID1517 | KR | BH1453 PROTEIN. |
| 55 | ID1518 | KR | BH1582 PROTEIN. |
| | ID1519 | KR | ORF starting with ATG of length 552 |
| | ID1520 | KT | LEXA REPRESSOR (EC 3.4.21.88) (SOS REGULATORY PROTEIN |
| | DINR) . | | |
| | ID1521 | KT | YVLC. |
| 60 | ID1522 | L | DNA POLYMERASE III POLC-TYPE (EC 2.7.7.7) (POLIII) . |
| | ID1523 | L | EXCINUCLEASE ABC SUBUNIT A. |
| | ID1524 | L | DNA POLYMERASE I (EC 2.7.7.7) (POL I) . |
| | ID1525 | L | ATP-DEPENDENT DNA HELICASE PCRA (EC 3.6.1.-) . |
| | ID1526 | L | MUTS2 PROTEIN. |
| 65 | ID1527 | L | EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN) . |
| | ID1528 | L | DNA GYRASE SUBUNIT B (EC 5.99.1.3) . |

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| | ID1529 | L | ATP-DEPENDENT NUCLEASE SUBUNIT A. |
| | ID1530 | L | Amino acid sequence of a DnaE polypeptide. |
| | ID1531 | L | DNA TOPOISOMERASE IV SUBUNIT A. |
| | ID1532 | L | PROBABLE DNA TOPOISOMERASE III (EC 5.99.1.2) |
| 5 | (RELAXING ENZY | | |
| | ID1533 | L | YIRY PROTEIN (PUTATIVE - HOMOLOGY WITH SBCC FROM C. |
| | PERFRING | | |
| | ID1534 | L | DNA GYRASE SUBUNIT A (EC 5.99.1.3). |
| | ID1535 | L | PRIMOSOMAL REPLICATION FACTOR Y. |
| 10 | ID1536 | L | DNA MISMATCH REPAIR PROTEIN MUTL.. |
| | ID1537 | L | YJCD PROTEIN. |
| | ID1538 | L | DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N). |
| | ID1539 | L | YRRC PROTEIN. |
| | ID1540 | L | YVGS PROTEIN. |
| 15 | ID1541 | L | PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG. |
| | ID1542 | L | DNA PRIMASE (EC 2.7.7.-). |
| | ID1543 | L | REPLICATIVE DNA HELICASE (EC 3.6.1.-). |
| | ID1544 | L | DNA MISMATCH REPAIR PROTEIN (MISMATCH RECOGNITION |
| | STEP). | | |
| 20 | ID1545 | L | YKOU PROTEIN. |
| | ID1546 | L | DNA TOPOISOMERASE IV SUBUNIT B. |
| | ID1547 | L | SPORE PHOTOPRODUCT LYASE. |
| | ID1548 | L | PROBABLE EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT (EC |
| 3.1.11.6 | | | |
| 25 | ID1549 | L | DNA POLYMERASE III SUBUNIT GAMMA/TAU (EC 2.7.7.7). |
| | ID1550 | L | REPLICATION INITIATION AND MEMBRANE ATTACHMENT |
| | PROTEIN. | | |
| | ID1551 | L | L.lactis HsdM subunit #2. |
| | ID1552 | L | EXCINUCLEASE ABC SUBUNIT C. |
| 30 | ID1553 | L | HYPOTHETICAL 47.0 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| | ID1554 | L | DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7). |
| | ID1555 | L | RECQ HOMOLOG. |
| | ID1556 | L | PROBABLE ENDONUCLEASE IV (EC 3.1.21.2) |
| 35 | (ENDODEOXYRIBONUCLEAS | | |
| | ID1557 | L | PROBABLE ATP-DEPENDENT HELICASE IN COTD-KDUD |
| | INTERGENIC REGI | | |
| | ID1558 | L | HYPOTHETICAL 40.5 KDA PROTEIN IN COMEC-RPST |
| | INTERGENIC REGIO | | |
| 40 | ID1559 | L | EXONUCLEASE SBCD HOMOLOG (FRAGMENT). |
| | ID1560 | L | CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA. |
| | ID1561 | L | PRIMOSOMAL PROTEIN DNAI. |
| | ID1562 | L | PROBABLE INTEGRASE/RECOMBINASE CODV. |
| | ID1563 | L | PUTATIVE DEOXYRIBONUCLEASE YABD (EC 3.1.21.-). |
| 45 | ID1564 | L | PUTATIVE 5'-3' EXONUCLEASE (EC 3.1.11.-). |
| | ID1565 | L | YFJP PROTEIN. |
| | ID1566 | L | HYPOTHETICAL 46.8 KDA PROTEIN. |
| | ID1567 | L | ORF starting with ATG of length 2277 |
| | ID1568 | L | FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23) |
| 50 | (FAPY-DNAG | | |
| | ID1569 | L | PROBABLE ENDONUCLEASE III (EC 4.2.99.18) (DNA- |
| | (APURINIC ORAP | | |
| | ID1570 | L | HYPOTHETICAL 37.4 KDA PROTEIN IN ACKA-SSPA INTERGENIC |
| | REGION | | |
| 55 | ID1571 | L | ATP-DEPENDENT DNA HELICASE RECQ (EC 3.6.1.-) |
| | (RECOMBINATION | | |
| | ID1572 | L | HOLLIDAY JUNCTION DNA HELICASE RUVB. |
| | ID1573 | L | DNA REPAIR PROTEIN RADC HOMOLOG. |
| | ID1574 | L | SA1093 PROTEIN. |
| 60 | ID1575 | L | HYPOTHETICAL 36.1 KDA PROTEIN IN SPOIIIC-CWLA |
| | INTERGENIC REG | | |
| | ID1576 | L | DNA REPAIR PROTEIN RECO (RECOMBINATION PROTEIN O). |
| | ID1577 | L | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDC. |
| | ID1578 | L | YOOV PROTEIN. |
| 65 | ID1579 | L | SIMILAR TO B. ANTHRACIS WEYAR ELEMENT ORFB. |

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| | ID1580 | L | PROBABLE ATP-DEPENDENT HELICASE IN COTD-KDUD |
| | INTERGENIC REGI | | |
| | ID1581 | L | YRVE PROTEIN. |
| 5 | ID1582 | L | Staphylococcus aureus CcrB1 protein sequence SEQ ID NO:8. |
| | ID1583 | L | YFHQ PROTEIN. |
| | ID1584 | L | ORF starting with ATG of length 1809 |
| | ID1585 | L | DNA GYRASE A (FRAGMENT). |
| 10 | ID1586 | L | UV-DAMAGE REPAIR PROTEIN. |
| | ID1587 | L | DNA REPLICATION AND REPAIR PROTEIN RECF. |
| | ID1588 | L | HYPOTHETICAL 48.0 KDA PROTEIN IN PONA-COTD INTERGENIC REGION |
| | ID1589 | L | ORF starting with ATG of length 1320 |
| 15 | ID1590 | L | TYPE IC RESTRICTION SUBUNIT. |
| | ID1591 | L | PROBABLE INTEGRASE/RECOMBINASE RIPX. |
| | ID1592 | L | SINGLE-STRAND DNA-SPECIFIC EXONUCLEASE. |
| | ID1593 | L | L.lactis HsdM subunit #1. |
| | ID1594 | L | PUTATIVE TYPE I RESTRICTION ENZYME R PROTEIN (EC 3.1.21.3). |
| 20 | ID1595 | L | YRVN PROTEIN. |
| | ID1596 | L | SIMILAR TO B. ANTHRACIS WEYAR ELEMENT ORFB. |
| | ID1597 | L | ORF starting with ATG of length 1146 |
| | ID1598 | L | ORF starting with ATG of length 1143 |
| | ID1599 | L | SA0828 PROTEIN. |
| 25 | ID1600 | L | HYPOTHETICAL 48.0 KDA PROTEIN IN PONA-COTD INTERGENIC REGION |
| | ID1601 | L | BH0056 PROTEIN. |
| | ID1602 | L | METALLOREGULATION DNA-BINDING STRESS PROTEIN. |
| | ID1603 | L | RECOMBINATION PROTEIN RECR. |
| 30 | ID1604 | L | YLBH PROTEIN. |
| | ID1605 | L | COME OPERON PROTEIN 1. |
| | ID1606 | L | METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1) |
| | ID1607 | L | YADA PROTEIN. |
| 35 | ID1608 | L | RIBONUCLEASE HII. |
| | ID1609 | L | DNA REPLICATION AND REPAIR PROTEIN RECF. |
| | ID1610 | L | SIMILAR TO E.COLI YJAF PROTEIN. |
| | ID1611 | L | 14.7 KDA RIBONUCLEASE H-LIKE PROTEIN. |
| 40 | ID1612 | L | EXTRACELLULAR RIBONUCLEASE PRECURSOR (EC 3.1.---). |
| | ID1613 | L | Amino acid sequence of a DnaE polypeptide. |
| | ID1614 | L | YUSF PROTEIN. |
| | ID1615 | L | ORF starting with ATG of length 1197 |
| | ID1616 | L | HOLLIDAY JUNCTION DNA HELICASE RUVA. |
| 45 | ID1617 | L | MISMATCH BINDING PROTEIN (FRAGMENT). |
| | ID1618 | L | ORF starting with ATG of length 774 |
| | ID1619 | L | SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX-DESTABILIZING PRO |
| | ID1620 | L | HYPOTHETICAL 15.2 KDA PROTEIN IN UDK-ALAS INTERGENIC REGION. |
| 50 | ID1621 | L | ORF starting with ATG of length 738 |
| | ID1622 | L | RECQ HOMOLOG. |
| | ID1623 | L | ATP-DEPENDENT DNA HELICASE RECQ (EC 3.6.1.-) |
| | (RECOMBINATION | | |
| | ID1624 | L | SIMILAR TO B. ANTHRACIS WEYAR ELEMENT ORFB. |
| 55 | ID1625 | L | YAZA PROTEIN. |
| | ID1626 | L | SIMILAR TO SINGLE STRAND BINDING PROTEIN. |
| | ID1627 | L | HYPOTHETICAL 43.5 KDA PROTEIN IN COTD-KDUD INTERGENIC REGION |
| | ID1628 | L | ORF starting with ATG of length 648 |
| 60 | ID1629 | L | ORF starting with ATG of length 645 |
| | ID1630 | L | HYPOTHETICAL 43.8 KDA PROTEIN. |
| | ID1631 | L | O6-METHYLGUANINE DNA ALKYLTRANSFERASE. |
| | ID1632 | L | ORF starting with ATG of length 606 |
| | ID1633 | L | DNA POLYMERASE III DELTA' SUBUNIT (EC 2.7.7.7). |
| 65 | ID1634 | L | YIRY PROTEIN (PUTATIVE - HOMOLOGY WITH SBCC FROM C. PERFRING |

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| | ID1635 | L | DNA-BINDING PROTEIN HU 1 (DNA-BINDING PROTEIN II) (HB). |
| | ID1636 | L | EXODEOXYRIBONUCLEASE VII (SMALL SUBUNIT). |
| | ID1637 | L | CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA. |
| 5 | ID1638 | L | Amino acid sequence of a DnaE polypeptide. |
| | ID1639 | L | SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX-DESTABILIZING PRO |
| | ID1640 | L | YNEB. |
| 10 | ID1641 | L | ORF starting with ATG of length 417 |
| | ID1642 | L | HYPOTHETICAL 17.0 KDA PROTEIN. |
| | ID1643 | L | EXCINUCLEASE ABC (C) (FRAGMENT). |
| | ID1644 | L | INT PROTEIN. |
| | ID1645 | L | RIBONUCLEASE HIIII (EC 3.1.26.-) (RNASE HIIII). |
| 15 | ID1646 | L | ORF starting with ATG of length 315 |
| | ID1647 | L | ORF starting with ATG of length 258 |
| | ID1648 | L | DNA HELICASE HOMOLOG (FRAGMENT). |
| | ID1649 | L | ORF starting with ATG of length 678 |
| | ID1650 | L | ORF starting with ATG of length 201 |
| | ID1651 | L | ORF starting with ATG of length 1143 |
| 20 | ID1652 | LK | TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF). |
| | ID1653 | LK | ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1.-). |
| | ID1654 | LK | TRANSCRIPTION-REPAIR COUPLING FACTOR (FRAGMENT). |
| | ID1655 | LK | ORF starting with ATG of length 657 |
| | ID1656 | LKJ | PROBABLE RNA HELICASE IN CCCA-SODA INTERGENIC REGION. |
| 25 | ID1657 | LKJ | COMF OPERON PROTEIN 1. |
| | ID1658 | LKJ | YFML PROTEIN. |
| | ID1659 | LKJ | COLD-SHOCK DEAD-BOX PROTEIN A HOMOLOG (ATP-DEPENDENT RNA HEL |
| | ID1660 | LKJ | HYPOTHETICAL 56.9 KDA PROTEIN. |
| 30 | ID1661 | LN | SMF PROTEIN. |
| | ID1662 | LR | Amino acid sequence of activator YgkG of methanol dehydrogen |
| | ID1663 | LR | MUTATOR MUTT PROTEIN. |
| | ID1664 | LR | MUTATOR MUTT PROTEIN. |
| 35 | ID1665 | LR | YTKD. |
| | ID1666 | M | STAGE V SPORULATION PROTEIN D (SPORULATION SPECIFIC PENICILL |
| | ID1667 | M | REGULATORY PROTEIN BLAR1. |
| | ID1668 | M | PENICILLIN-BINDING PROTEIN 1F (PBP-1F). |
| 40 | ID1669 | M | GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZ |
| | ID1670 | M | PENICILLIN-BINDING PROTEIN 2B (PBP-2B). |
| | ID1671 | M | PENICILLIN-BINDING PROTEIN 1A/1B (PBP1) [INCLUDES: PENICILLI |
| 45 | ID1672 | M | HYPOTHETICAL 71.8 KDA PROTEIN. |
| | ID1673 | M | PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PBP 4). |
| | ID1674 | M | PENICILLIN-BINDING PROTEIN 3 (PBP 3) (PSPB20). |
| | ID1675 | M | YFLE PROTEIN. |
| | ID1676 | M | YRRR PROTEIN. |
| 50 | ID1677 | M | UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE 1 (EC 2.5. |
| | ID1678 | M | TEICHOIC ACID BIOSYNTHESIS PROTEIN F. |
| | ID1679 | M | UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE 2 (EC 2.5. |
| 55 | ID1680 | M | HYPOTHETICAL 73.6 KDA PROTEIN IN DNAC-RPLI INTERGENIC REGION |
| | ID1681 | M | YVGJ PROTEIN. |
| | ID1682 | M | D-ALANYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) |
| 60 | ID1683 | M | PROBABLE N-ACETYLMURAMOYL-L-ALANINE AMIDASE PRECURSOR (EC 3. |
| | ID1684 | M | B. subtilis yaeL polypeptide. |
| | ID1685 | M | UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE (EC 6.3.2.9) |
| 65 | ID1686 | M | HYPOTHETICAL 73.2 KDA PROTEIN IN SODA-COMGA INTERGENIC REGIO |

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| | ID1687 | M | CARBOXY-TERMINAL PROCESSING PROTEASE. |
| | ID1688 | M | SPOIVB. |
| | ID1689 | M | B. subtilis glycosyl transferase catalytic domain. |
| | ID1690 | M | DLTB PROTEIN. |
| 5 | ID1691 | M | PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A). |
| | ID1692 | M | GCPE PROTEIN HOMOLOG. |
| | ID1693 | M | PENICILLIN-BINDING PROTEIN DACF PRECURSOR (D-ALANYL- |
| | D-ALANIN | | |
| 10 | ID1694 | M | UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL- (PENTAPEPTIDE) PYROP |
| | ID1695 | M | HYPOTHETICAL 42.0 KDA PROTEIN IN DAPB-PAPS INTERGENIC REGION |
| | ID1696 | M | PUTATIVE UNDECAPRENYL-PHOSPHATE N- ACETYLGLUCOSAMINYLTRANSFER |
| 15 | ID1697 | M | UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) (N-A |
| | ID1698 | M | YBVE PROTEIN (YBZA). |
| | ID1699 | M | UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6- DIAMINOPIMELATE L |
| 20 | ID1700 | M | YKUA PROTEIN. |
| | ID1701 | M | UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9) (U |
| | ID1702 | M | HYPOTHETICAL 43.6 KDA PROTEIN. |
| | ID1703 | M | GLYCINE BETAINE/CARNITINE/CHOLINE-BINDING PROTEIN |
| 25 | PRECURSOR (| | |
| | ID1704 | M | CSBB PROTEIN. |
| | ID1705 | M | TUAH PROTEIN. |
| | ID1706 | M | SIMILAR TO E.COLI NLPC PROTEIN AND TO LISTERIA SPECIES P60-R |
| 30 | ID1707 | M | TUAC PROTEIN. |
| | ID1708 | M | YFNI. |
| | ID1709 | M | BETA-LACTAMASE (EC 3.5.2.6) (PENICILLINASE) (CEPHALOSPORINAS |
| | ID1710 | M | HYPOTHETICAL 37.4 KDA PROTEIN IN SPOIIASA-HTRA INTERGENIC REG |
| 35 | ID1711 | M | HYPOTHETICAL 50.1 KDA PROTEIN. |
| | ID1712 | M | YKON. |
| | ID1713 | M | N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLM (EC 3.5.1.28) (CELL |
| 40 | ID1714 | M | PUTATIVE ALANINE RACEMASE (EC 5.1.1.1). |
| | ID1715 | M | HYPOTHETICAL 42.6 KDA PROTEIN. |
| | ID1716 | M | UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2). |
| | ID1717 | M | GALE. |
| | ID1718 | M | HYPOTHETICAL 38.5 KDA PROTEIN IN TNRA-SSPD INTERGENIC REGION |
| 45 | ID1719 | M | HYPOTHETICAL 37.2 KDA PROTEIN IN IDH-DEOR INTERGENIC REGION. |
| | ID1720 | M | YKCB PROTEIN. |
| | ID1721 | M | GLUTAMATE RACEMASE (EC 5.1.1.3). |
| 50 | ID1722 | M | GENERAL STRESS PROTEIN A. |
| | ID1723 | M | HYPOTHETICAL 40.6 KDA PROTEIN IN SPOVID 3'REGION (ORF2). |
| | ID1724 | M | ORF starting with ATG of length 2235 |
| | ID1725 | M | PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC |
| 55 | 2.4.99.-) (SPO | | |
| | ID1726 | M | SPORE-CORTEX-LYTIC ENZYME PRECURSOR. |
| | ID1727 | M | HYPOTHETICAL 80.1 KDA PROTEIN IN SODA-COMGA INTERGENIC REGIO |
| | ID1728 | M | HYPOTHETICAL 32.7 KDA PROTEIN. |
| 60 | ID1729 | M | ROD SHAPE-DETERMINING PROTEIN MREC. |
| | ID1730 | M | ALPHA-D-MANNOSE-ALPHA(1-6) PHOSPHATIDYL MYO-INOSITOL MONOMANN |
| | ID1731 | M | TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR. |
| | ID1732 | M | YUSA PROTEIN. |
| 65 | ID1733 | M | GERMINATION-SPECIFIC N-ACETYLMURAMOYL-L-ALANINE AMIDASE (EC |

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| | ID1734 | M | TUAG PROTEIN. |
| | ID1735 | M | DIVIB PROTEIN. |
| | ID1736 | M | HYPOTHETICAL 24.4 KDA PROTEIN. |
| 5 | ID1737 | M | HYPOTHETICAL 42.5 KDA PROTEIN IN CITA-SSPB INTERGENIC REGION |
| | ID1738 | M | HYPOTHETICAL 39.8 KDA PROTEIN. |
| | ID1739 | M | ORF starting with ATG of length 1982 |
| | ID1740 | M | CARBOXYPEPTIDASE. |
| 10 | ID1741 | M | PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8.) |
| | ID1742 | M | YKFC. |
| | ID1743 | M | GALE. |
| | ID1744 | M | 455AA LONG HYPOTHETICAL VI POLYSACCHARIDE BIOSYNTHESIS PROTE |
| 15 | ID1745 | M | Bacillus subtilis IFO 3336 PGA synthesising enzyme. |
| | ID1746 | M | YRVJ PROTEIN. |
| | ID1747 | M | D-alanine racemase from Bacillus licheniformis. |
| | ID1748 | M | UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158) |
| 20 | ID1749 | M | PLEIOTROPIC REGULATORY PROTEIN. |
| | ID1750 | M | PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE) |
| | ID1751 | M | CARBOXY-TERMINAL PROCESSING PROTEASE. |
| 25 | ID1752 | M | STAGE IV SPORULATION PROTEIN FA. |
| | ID1753 | M | PUTATIVE PENICILLIN BINDING PROTEIN PRECURSOR. |
| | ID1754 | M | ENDOPEPTIDASE LYTF PRECURSOR (CELL WALL-ASSOCIATED POLYPEPTI |
| | ID1755 | M | ORF starting with ATG of length 1527 |
| 30 | ID1756 | M | HYPOTHETICAL 23.1 KDA PROTEIN. |
| | ID1757 | M | ORF starting with ATG of length 1497 |
| | ID1758 | M | D-ALANINE--D-ALANINE LIGASE (EC 6.3.2.4) (D-ALANYLALANINE SY |
| | ID1759 | M | YUNA PROTEIN. |
| 35 | ID1760 | M | PUTATIVE ENDOPEPTIDASE LYTE PRECURSOR (PHOSPHATASE-ASSOCIATE |
| | ID1761 | M | HYPOTHETICAL 35.3 KDA PROTEIN IN FTSL 5'REGION (ORFB). |
| | ID1762 | M | GALE. |
| | ID1763 | M | ORF46. |
| 40 | ID1764 | M | D-ALANINE--D-ALANINE LIGASE (EC 6.3.2.4) (D-ALANYLALANINE SY |
| | ID1765 | M | SIMILAR TO PSEUDOMONAS AERUGINOSA GDP-MANNOSE 6-DEHYDROGENAS |
| 45 | ID1766 | M | HYPOTHETICAL 22.2 KDA PROTEIN IN SPO0A-MMGA INTERGENIC REGIO |
| | ID1767 | M | YUNA PROTEIN. |
| | ID1768 | M | HYPOTHETICAL 80.1 KDA PROTEIN IN SODA-COMGA INTERGENIC REGIO |
| | ID1769 | M | UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6- |
| 50 | DIAMINOPIMELATE-D- | | |
| | ID1770 | M | ORF starting with ATG of length 1236 |
| | ID1771 | M | ORF starting with ATG of length 1227 |
| | ID1772 | M | N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLL PRECURSOR (EC 3.5.1. |
| 55 | ID1773 | M | MINIMAL CHANGE NEPHRITIS TRANSMEMBRANE GLYCOPROTEIN (FRAGMEN |
| | ID1774 | M | ORF starting with ATG of length 1170 |
| | ID1775 | M | GLUCOSE INHIBITED DIVISION PROTEIN B. |
| | ID1776 | M | ROD SHAPE-DETERMINING PROTEIN MRED. |
| 60 | ID1777 | M | SIMILAR TO BACILLUS ANTHRACIS CAPA PROTEIN. |
| | ID1778 | M | TEICOIC ACID BIOSYNTHESIS PROTEIN A. |
| | ID1779 | M | N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLM (EC 3.5.1.28) (CELL |
| | ID1780 | M | YTMP. |
| 65 | ID1781 | M | HYPOTHETICAL 25.8 KDA PROTEIN IN EPR-GALK INTERGENIC REGION. |

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| | ID1782 | M | ORF starting with ATG of length 1062 |
| | ID1783 | M | GLYCINE BETAINE TRANSPORTER OPUD. |
| | ID1784 | M | ORF starting with ATG of length 1035 |
| | ID1785 | M | YNGB PROTEIN. |
| 5 | ID1786 | M | PLEIOTROPIC REGULATORY PROTEIN DEGT. |
| | ID1787 | M | STAGE V SPORULATION PROTEIN G. |
| | ID1788 | M | UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23). |
| | ID1789 | M | LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL. |
| 10 | ID1790 | M | STAGE II SPORULATION PROTEIN. |
| | ID1791 | M | B. subtilis hexulose phosphate isomerase. |
| | ID1792 | M | UDP-D-GLUCOSE-DEHYDROGENASE GDHGA. |
| | ID1793 | M | YNGB PROTEIN. |
| 15 | ID1794 | M | Amino acid sequence of epsH of L. delbrueckii bulgaricus Lfi |
| | ID1795 | M | PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) (|
| | ID1796 | M | N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLL PRECURSOR (EC 3.5.1. |
| 20 | ID1797 | M | ORF starting with ATG of length 810 |
| | ID1798 | M | BH1600 PROTEIN. |
| | ID1799 | M | PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) (|
| | ID1800 | M | ORF starting with ATG of length 753 |
| 25 | ID1801 | M | PENICILLIN-BINDING PROTEIN 1A/1B (PBP1) [INCLUDES: PENICILLI |
| | ID1802 | M | Staphylococcus aureus ica A protein. |
| | ID1803 | M | TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG. |
| | ID1804 | M | PUTATIVE ALANINE RACEMASE (EC 5.1.1.1). |
| 30 | ID1805 | M | ORF starting with ATG of length 654 |
| | ID1806 | M | PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8. |
| | ID1807 | M | HYPOTHETICAL 73.2 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| 35 | ID1808 | M | TUAA PROTEIN. |
| | ID1809 | M | HYPOTHETICAL 18.4 KDA PROTEIN. |
| | ID1810 | M | AMIDASE ENHANCER PRECURSOR (MODIFIER PROTEIN OF MAJOR AUTOLY |
| | ID1811 | M | PENICILLIN-BINDING PROTEIN 2B (INTERNAL REGION OF THE |
| 40 | PENICIL | | CWLV. |
| | ID1812 | M | UDP-N-AACERYLMURAMATE-ALANINE LIGASE. |
| | ID1813 | M | ORF starting with ATG of length 498 |
| | ID1814 | M | PHOSPHINOTHRICIN N-ACETYLTRANSFERASE. |
| 45 | ID1815 | M | ORF starting with ATG of length 495 |
| | ID1816 | M | ORF starting with ATG of length 483 |
| | ID1817 | M | TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG. |
| | ID1818 | M | AMIDASE ENHANCER PRECURSOR (MODIFIER PROTEIN OF MAJOR AUTOLY |
| | ID1819 | M | |
| 50 | ID1820 | M | MurF protein. |
| | ID1821 | M | HYPOTHETICAL 40.8 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| | ID1822 | M | GLYCINE BETAINE TRANSPORTER OPUD. |
| | ID1823 | M | ORF starting with ATG of length 372 |
| 55 | ID1824 | M | ORF starting with TTG or GTG of length 705 |
| | ID1825 | M | ORF starting with ATG of length 327 |
| | ID1826 | M | HYPOTHETICAL 30.5 KDA PROTEIN. |
| | ID1827 | M | ORF starting with ATG of length 276 |
| | ID1828 | MG | HYPOTHETICAL 66.3 KDA PROTEIN. |
| 60 | ID1829 | MG | HYPOTHETICAL 28.2 KDA PROTEIN IN BIOI 3'REGION (ORF2). |
| | ID1830 | MG | PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDEN |
| | ID1831 | MG | HYPOTHETICAL 66.3 KDA PROTEIN. |
| 65 | ID1832 | MG | ORF starting with ATG of length 975 |
| | ID1833 | MG | CONSERVED HYPOTHETICAL PROTEIN. |

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| | ID1834 | MG | PUTATIVE SUGAR NUCLEOTIDE BIOSYNTHESIS PROTEIN. |
| | ID1835 | MG | YESF PROTEIN. |
| | ID1836 | N | GTP-BINDING PROTEIN LEPA. |
| | ID1837 | N | GTP-BINDING PROTEIN TYPa/BIPA HOMOLOG. |
| 5 | ID1838 | N | PREPROTEIN TRANSLOCASE SECA SUBUNIT. |
| | ID1839 | N | CHEMOTAXIS PROTEIN CHEA (EC 2.7.3.-). |
| | ID1840 | N | B. subtilis secretion factor SecDF. |
| | ID1841 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN MCPA (H1). |
| | ID1842 | N | YOAH. |
| 10 | ID1843 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN MCPB (H3). |
| | ID1844 | N | PREPROTEIN TRANSLOCASE SECY SUBUNIT. |
| | ID1845 | N | FLAGELLUM-SPECIFIC ATP SYNTHASE (EC 3.6.1.34). |
| | ID1846 | N | FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1). |
| 15 | ID1847 (HOMOLOG). | N | SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR |
| | ID1848 | N | FLAGELLAR HOOK-ASSOCIATED PROTEIN 2 (HAP2) (FILAMENT |
| | CAP PRO | | |
| | ID1849 | N | FLAGELLAR MOTOR SWITCH PROTEIN FLIG. |
| | ID1850 | N | HYPOTHETICAL 48.8 KDA PROTEIN. |
| 20 | ID1851 | N | FLAGELLAR BIOSYNTHETIC PROTEIN FLHB. |
| | ID1852 | N | Bacillus subtilis protein secretion chaperone FtsY. |
| | ID1853 | N | FLAGELLAR BIOSYNTHESIS PROTEIN FLHA. |
| | ID1854 | N | COMG OPERON PROTEIN 1. |
| | ID1855 | N | FLAGELLIN. |
| 25 | ID1856 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN MCPB (H3). |
| | ID1857 | N | FLAGELLAR M-RING PROTEIN. |
| | ID1858 | N | CHEMOTAXIS CHEV PROTEIN (EC 2.7.3.-). |
| | ID1859 | N | FLAGELLAR HOOK-ASSOCIATED PROTEIN 3 (HAP3). |
| | ID1860 | N | YFMS. |
| 30 | ID1861 | N | FLAGELLA-ASSOCIATED PROTEIN. |
| | ID1862 | N | FLAGELLAR MOTOR SWITCH PROTEIN. |
| | ID1863 (ORFA). | N | HYPOTHETICAL 30.1 KDA PROTEIN IN ACUC 5'REGION |
| | ID1864 | N | FLAGELLAR BIOSYNTHESIS PROTEIN FLHF (FLAGELLA |
| 35 | ASSOCIATED GTP | | |
| | ID1865 | N | CHEMOTAXIS MOTA PROTEIN (MOTILITY PROTEIN A). |
| | ID1866 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPC. |
| | ID1867 | N | FLAGELLAR BIOSYNTHETIC PROTEIN FLIR. |
| | ID1868 | N | FLAGELLAR BIOSYNTHETIC PROTEIN FLIP. |
| 40 | ID1869 | N | ORF starting with ATG of length 1983 |
| | ID1870 | N | FLAGELLAR HOOK-BASAL BODY COMPLEX PROTEIN FLHO. |
| | ID1871 | N | COMG OPERON PROTEIN 2. |
| | ID1872 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN MCPC. |
| | ID1873 | N | ORF starting with ATG of length 1785 |
| 45 | ID1874 | N | ORF starting with ATG of length 1734 |
| | ID1875 | N | ORF starting with ATG of length 1725 |
| | ID1876 | N | HYPOTHETICAL 28.1 KDA PROTEIN IN PHOD-PCP INTERGENIC |
| | REGION | | |
| | ID1877 | N | FLAGELLAR HOOK-BASAL BODY COMPLEX PROTEIN FLHP. |
| 50 | ID1878 | N | SECDF PROTEIN (PROTEIN-EXPORT MEMBRANE PROTEIN). |
| | ID1879 | N | STAGE III SPORULATION PROTEIN J PRECURSOR. |
| | ID1880 | N | ORF starting with ATG of length 1566 |
| | ID1881 | N | HYPOTHETICAL 30.7 KDA LIPOPROTEIN IN GLNQ-ANSR |
| 55 | INTERGENIC RE | | |
| | ID1882 | N | ORF39. |
| | ID1883 | N | PROBABLE FLAGELLAR HOOK-LENGTH CONTROL PROTEIN. |
| | ID1884 | N | Amino acid sequence of a SipW protein of Bacillus |
| | subtilis. | | |
| | ID1885 | N | TYPE 4 PREPILIN-LIKE PROTEINS LEADER PEPTIDE |
| 60 | PROCESSING ENZY | | |
| | ID1886 | N | FLAGELLAR FLIJ PROTEIN (CHEMOTAXIS CHEF PROTEIN). |
| | ID1887 | N | SIGNAL PEPTIDASE TYPE I. |
| | ID1888 | N | FLAGELLAR BASAL-BODY ROD PROTEIN FLGG (DISTAL ROD |
| | PROTEIN). | | |
| 65 | ID1889 (ORF2). | N | HYPOTHETICAL 24.6 KDA PROTEIN IN CCPA 3'REGION |

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| | | | CHEMOTAXIS PROTEIN CHEW. |
| | | | FLAGELLAR PROTEIN FLIS. |
| | | | HYPOTHETICAL 29.1 KDA PROTEIN IN PHOB-GROES |
| | | INTERGENIC REGIO | |
| 5 | ID1893 | N | YOCH. |
| | ID1894 | N | ORF starting with ATG of length 964 |
| | ID1895 | N | ORF starting with ATG of length 954 |
| | ID1896 | N | FLAGELLAR FLIL PROTEIN. |
| 10 | ID1897 | N | PREPROTEIN TRANSLOCASE SECA SUBUNIT (FRAGMENT). |
| | ID1898 | N | SIGNAL PEPTIDASE I (EC 3.4.21.89) (SPASE I) (LEADER PEPTIDASE) |
| | ID1899 | N | FLAGELLAR BIOSYNTHETIC PROTEIN FLIQ. |
| | ID1900 | N | FLAGELLAR ASSEMBLY PROTEIN. |
| 15 | ID1901 | N | HYPOTHETICAL 9.9 KDA PROTEIN IN SPOVB-TGT INTERGENIC REGION. |
| | ID1902 | N | MOTILITY PROTEIN. |
| | ID1903 | N | COMG OPERON PROTEIN 3 PRECURSOR. |
| | ID1904 | N | ORF starting with ATG of length 620 |
| 20 | ID1905 | N | FLAGELLAR BASAL-BODY ROD PROTEIN FLGB. |
| | ID1906 | N | HYPOTHETICAL 13.0 KDA PROTEIN IN HAG-FLID INTERGENIC REGION |
| | ID1907 | N | FLAGELLAR BASAL-BODY ROD PROTEIN FLGC. |
| | ID1908 | N | YRBA PROTEIN. |
| 25 | ID1909 | N | PREPROTEIN TRANSLOCASE SECA SUBUNIT. |
| | ID1910 | N | ORF starting with ATG of length 399 |
| | ID1911 | N | ORF starting with ATG of length 336 |
| | ID1912 | N | ORF starting with ATG of length 314 |
| | ID1913 | N | THA4 PROTEIN PRECURSOR. |
| 30 | ID1914 | NO | HYPOTHETICAL 46.5 KDA PROTEIN IN RPSU-PHOH |
| | ID1915 | NO | PROTEINASE IV. |
| | ID1916 | NO | BH2397 PROTEIN. |
| | ID1917 | NO | PUTATIVE PROTEASE/SCAFFOLD PROTEIN. |
| 35 | ID1918 | NT | FLAGELLAR MOTOR SWITCH PROTEIN FLIY. |
| | ID1919 | NT | PROTEIN-GLUTAMATE METHYLESTERASE (EC 3.1.1.61). |
| | ID1920 | NT | CHEMOTAXIS PROTEIN METHYLTRANSFERASE (EC 2.1.1.80). |
| | ID1921 | NT | CHEMOTAXIS PROTEIN CHEC. |
| | ID1922 | NT | CHEMOTAXIS PROTEIN CHED. |
| 40 | ID1923 | NT | CHEMOTAXIS PROTEIN CHEC. |
| | ID1924 | NT | ORF starting with ATG of length 321 |
| | ID1925 | O | BACILLOPEPTIDASE F PRECURSOR (EC 3.4.21.-) (ESTERASE) |
| | (RP-I | | |
| | ID1926 | O | NEGATIVE REGULATOR OF GENETIC COMPETENCE CLPC/MECB. |
| | ID1927 | O | TRANSCRIPTIONAL REGULATORY PROTEIN LEVR. |
| 45 | ID1928 | O | B. subtilis FtsH protein. |
| | ID1929 | O | ATP-DEPENDENT CLP PROTEASE-LIKE. |
| | ID1930 | O | ATP-DEPENDENT PROTEASE LA HOMOLOG (EC 3.4.21.-). |
| | ID1931 | O | RESB PROTEIN. |
| | ID1932 | O | ATP-DEPENDENT PROTEASE LA 1 (EC 3.4.21.53). |
| 50 | ID1933 | O | MINOR EXTRACELLULAR PROTEASE VPR PRECURSOR (EC 3.4.21.-). |
| | ID1934 | O | ALKALINE SERINE PROTEASE. |
| | ID1935 | O | CELL WALL-ASSOCIATED PROTEASE PRECURSOR (EC 3.4.21.-) |
| | [CONTA | | |
| 55 | ID1936 | O | DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMO) |
| | ID1937 | O | THIOREDOXINE REDUCTASE. |
| | ID1938 | O | BACILLOPEPTIDASE F PRECURSOR (EC 3.4.21.-) (ESTERASE) |
| | (RP-I | | |
| 60 | ID1939 | O | ARGININE UTILIZATION REGULATORY PROTEIN ROCR. |
| | ID1940 | O | STAGE V SPORULATION PROTEIN K. |
| | ID1941 | O | RESC PROTEIN. |
| | ID1942 | O | HTRA-LIKE SERINE PROTEASE. |
| | ID1943 | O | YRRO PROTEIN. |
| 65 | ID1944 | O | HYPOTHETICAL PROTEASE IN ROCR-PURA INTERGENIC REGION (EC 3.4 |

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| | ID1945 | O | HYPOTHETICAL 36.3 KDA PROTEIN IN RECQ-CMK INTERGENIC REGION. |
| | ID1946 | O | ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT (CLASS III HE) |
| 5 | ID1947 | O | 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (STRESS PR) |
| | ID1948 | O | HEMX PROTEIN. |
| | ID1949 | O | MINOR EXTRACELLULAR PROTEASE EPR PRECURSOR (EC 3.4.21.-). |
| 10 | ID1950 | O | ATP-DEPENDENT CLP PROTEASE (HEAT-SHOCK PROTEIN). |
| | ID1951 | O | CELL DIVISION CYCLE PROTEIN. |
| | ID1952 | O | HEAT SHOCK PROTEIN HTPG. |
| | ID1953 | O | TRIGGER FACTOR (TF) (VEGETATIVE PROTEIN 2) (VEG2). |
| | ID1954 | O | CHAPERONE PROTEIN DNAJ. |
| 15 | ID1955 | O | YKVL PROTEIN. |
| | ID1956 | O | PUTATIVE METALLOPROTEASE YHFN (EC 3.4.24.-) (PSP23). |
| | ID1957 | O | Bacillus megaterium HSP (Bmehsp70). |
| | ID1958 | O | ALKYL HYDROPEROXIDE REDUCTASE C22 PROTEIN (EC 1.6.4.-) (GENE) |
| 20 | ID1959 | O | ORF starting with ATG of length 1665 |
| | ID1960 | O | Bacillus megaterium HSP (Bmehsp70). |
| | ID1961 | O | ATP-DEPENDENT PROTEASE HSLV PRECURSOR (EC 3.4.99.-). |
| | ID1962 | O | ALKYL HYDROPEROXIDE REDUCTASE LARGE SUBUNIT (EC 1.6.99.3) (P) |
| 25 | ID1963 | O | CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA. |
| | ID1964 | O | PUTATIVE SIGMA L-DEPENDENT TRANSCRIPTIONAL REGULATOR IN DFRA |
| | ID1965 | O | YKDA. |
| 30 | ID1966 | O | 33 KDA CHAPERONIN (HEAT SHOCK PROTEIN 33 HOMOLOG) (HSP33). |
| | ID1967 | O | PEPTIDE METHIONINE SULFOXIDE REDUCTASE (EC 1.8.4.6) (PROTEIN) |
| | ID1968 | O | YVGV PROTEIN. |
| | ID1969 | O | YVJD. |
| 35 | ID1970 | O | SA2162 PROTEIN. |
| | ID1971 | O | YVGU PROTEIN. |
| | ID1972 | O | HYPOTHETICAL 16.6 KDA PROTEIN IN MSRA 3'REGION. |
| | ID1973 | O | Bacillus carlsberg alkaline elastase. |
| | ID1974 | O | PROTEIN EXPORT PROTEIN PRSA PRECURSOR. |
| 40 | ID1975 | O | HYPOTHETICAL 25.2 KDA PROTEIN. |
| | ID1976 | O | GLUTATHIONE PEROXIDASE HOMOLOG BSAA. |
| | ID1977 | O | Arabidopsis thaliana protein fragment SEQ ID NO: 56671. |
| | ID1978 | O | CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA. |
| 45 | ID1979 | O | GENERAL STRESS PROTEIN 170 (GSP170). |
| | ID1980 | O | YMAD PROTEIN. |
| | ID1981 | O | YVJD. |
| | ID1982 | O | GRPE PROTEIN (HSP-70 COFACTOR). |
| | ID1983 | O | SUBTILISIN CARLSBERG PRECURSOR (EC 3.4.21.62). |
| 50 | ID1984 | O | THIOL PROTEASE |
| | ID1985 | O | PLASMID PAD1 (FROM ENTEROCOCCUS FAECALIS) CYLLL, CYLLS, CYLM |
| | ID1986 | O | Staphylococcus aureus glycoprotease (gcp) protein. |
| | ID1987 | O | Amino acid sequence of a heat shock protein. |
| 55 | ID1988 | O | FORMATE ACETYLTRANSFERASE ACTIVATING ENZYME. |
| | ID1989 | O | YUTI PROTEIN. |
| | ID1990 | O | ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU. |
| | ID1991 | O | ORF starting with ATG of length 750 |
| | ID1992 | O | SPORE COAT PROTEIN M. |
| 60 | ID1993 | O | ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT (CLASS III HE) |
| | ID1994 | O | 10 KDA CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES). |
| | ID1995 | O | ANAEROBIC RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE ACTIVATING P |
| 65 | ID1996 | O | PUTATIVE METALLOPROTEASE YHFN (EC 3.4.24.-) (PSP23). |
| | ID1997 | O | BACTERIOFERRITIN COMIGRATORY PROTEIN HOMOLOG. |

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| | ID1998 | O | PYRROLIDONE-CARBOXYLATE PEPTIDASE (EC 3.4.19.3) (5- |
| | OXOPROLYL | | |
| | ID1999 | O | Bacillus megaterium HSP (Bmehsp70). |
| | ID2000 | O | CHAPERONE HSLU. |
| 5 | ID2001 | O | ORF starting with ATG of length 498 |
| | ID2002 | O | HYPOTHETICAL 16.3 kDa PROTEIN IN PONA-COTD INTERGENIC |
| | REGION | | |
| | ID2003 | O | SMALL PROTEIN B HOMOLOGUE. |
| | ID2004 | O | ALKYL HYDROPEROXIDE REDUCTASE LARGE SUBUNIT (EC |
| 10 | 1.6.99.3) (P | | |
| | ID2005 | O | PYRUVATE FORMATE-LYASE ACTIVATING ENZYME (EC |
| | 1.97.1.4) (PFL- | | |
| | ID2006 | O | ORF starting with ATG of length 276 |
| | ID2007 | O | ATP-DEPENDENT PROTEASE LA 1 (EC 3.4.21.53). |
| 15 | ID2008 | OC | RESA PROTEIN. |
| | ID2009 | OC | YKVV PROTEIN. |
| | ID2010 | OC | PUTATIVE THIOREDOXIN. |
| | ID2011 | OC | YDFQ PROTEIN. |
| | ID2012 | OC | YNEN PROTEIN. |
| 20 | ID2013 | OC | YUSE PROTEIN. |
| | ID2014 | OC | Thioredoxin-Treponema pallidum 15 kDa antigen fusion |
| | protein | | |
| | ID2015 | OC | ORF starting with ATG of length 219 |
| | ID2016 | P | YLOB PROTEIN. |
| 25 | ID2017 | P | POTENTIAL COPPER-TRANSPORTING ATPASE (EC 3.6.3.4). |
| | ID2018 | P | SULFITE REDUCTASE (NADPH). |
| | ID2019 | P | ALKALINE PHOSPHATASE D PRECURSOR (EC 3.1.3.1) |
| | (APASED) (RAN1 | | |
| | ID2020 | P | YKVV PROTEIN. |
| 30 | ID2021 | P | HYPOTHETICAL 57.4 kDa PROTEIN. |
| | ID2022 | P | CATALASE HPII. |
| | ID2023 | P | Amino acid sequence of a Bacillus P450 monooxygenase |
| | protein | | |
| | ID2024 | P | SULFATE PERMEASE. |
| 35 | ID2025 | P | Alkaline phosphatase. |
| | ID2026 | P | NA+-TRANSPORTING ATP SYNTHASE. |
| | ID2027 | P | NA+/H+ ANTIPORTER. |
| | ID2028 | P | CHROMATE TRANSPORTER. |
| | ID2029 | P | PUTATIVE NITRATE REDUCTASE BETA CHAIN. |
| 40 | ID2030 | P | YJBQ PROTEIN. |
| | ID2031 | P | YFKE PROTEIN. |
| | ID2032 | P | FEQB PROTEIN. |
| | ID2033 | P | CATALASE X (EC 1.11.1.6). |
| | ID2034 | P | NA+-TRANSPORTING ATP SYNTHASE. |
| 45 | ID2035 | P | HOMOLOGUE OF COPPER EXPORT PROTEIN PCOD OF E. COLI. |
| | ID2036 | P | YLNA PROTEIN. |
| | ID2037 | P | SULFITE REDUCTASE (NADPH). |
| | ID2038 | P | PROBABLE LOW-AFFINITY INORGANIC PHOSPHATE |
| | TRANSPORTER. | | |
| 50 | ID2039 | P | NITRITE EXTRUSION PROTEIN (NITRITE FACILITATOR). |
| | ID2040 | P | FERRICHROME-BINDING PROTEIN PRECURSOR. |
| | ID2041 | P | YKOK. |
| | ID2042 | P | BH1407 PROTEIN. |
| | ID2043 | P | PROBABLE AMMONIUM TRANSPORTER (MEMBRANE PROTEIN |
| 55 | NRGA). | | |
| | ID2044 | P | IRON-UPTAKE SYSTEM BINDING PROTEIN PRECURSOR. |
| | ID2045 | P | YFJQ PROTEIN. |
| | ID2046 | P | YVGW PROTEIN. |
| | ID2047 | P | MANGANESE-CONTAINING CATALASE. |
| 60 | ID2048 | P | NITRATE TRANSPORTER. |
| | ID2049 | P | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN |
| | YQGK. | | |
| | ID2050 | P | YKOY PROTEIN. |
| | ID2051 | P | YBAF PROTEIN. |
| 65 | ID2052 | P | PROBABLE SUPEROXIDE DISMUTASE [FE] (EC 1.15.1.1). |
| | ID2053 | P | HYPOTHETICAL 57.2 kDa PROTEIN. |

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| | ID2054 | P | YTLD. |
| | ID2055 | P | SULFATE ADENYLYLTRANSFERASE (EC 2.7.7.4) (SULFATE |
| | ADENYLATE TET | | |
| 5 | ID2056 | P | HYPOTHETICAL 33.4 KDA PROTEIN IN DNAJ-RPSU |
| | INTERGENIC REGIO | | |
| | ID2057 | P | YLMA PROTEIN. |
| | ID2058 | P | HYPOTHETICAL 23.8 KDA PROTEIN IN SPOIIASA-HTRA |
| | INTERGENIC REG | | |
| 10 | ID2059 | P | HYPOTHETICAL 31.8 KDA PROTEIN IN GABP-GUAA INTERGENIC |
| | REGION | | |
| | ID2060 | P | HYPOTHETICAL 29.2 KDA PROTEIN IN RAPJ-OPUAA |
| | INTERGENIC REGIO | | |
| | ID2061 | P | FERRIC ANGUIBACTIN-BINDING PROTEIN PRECUSOR FABE OF |
| | V. ANGUI | | |
| 15 | ID2062 | P | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN |
| | YBXA. | | |
| | ID2063 | P | YKRM PROTEIN. |
| | ID2064 | P | HYPOTHETICAL 24.3 KDA PROTEIN IN KINC-ADEC INTERGENIC |
| | REGION | | |
| 20 | ID2065 | P | PROBABLE ABC TRANSPORTER BINDING PROTEIN YQGG |
| | PRECURSOR. | | |
| | ID2066 | P | HYPOTHETICAL 38.6 KDA PROTEIN. |
| | ID2067 | P | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN FEUA-SIGW |
| | INTERGEN | | |
| 25 | ID2068 | P | YFIY PROTEIN. |
| | ID2069 | P | COTJC PROTEIN. |
| | ID2070 | P | SA0587 PROTEIN. |
| | ID2071 | P | YLNA PROTEIN. |
| | ID2072 | P | HYPOTHETICAL 37.7 KDA PROTEIN IN SODA-COMGA |
| 30 | INTERGENIC REGIO | | |
| | ID2073 | P | PROBABLE MANGANESE TRANSPORT PROTEIN MNTH. |
| | ID2074 | P | PROBABLE ADENYLYLSULFATE KINASE (EC 2.7.1.25) (APS |
| | KINASE) (| | |
| | ID2075 | P | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGI. |
| 35 | ID2076 | P | CYTOCHROME B SUBUNIT OF NITRIC OXIDE REDUCTASE. |
| | ID2077 | P | SUPEROXIDE DISMUTASE (EC 1.15.1.1). |
| | ID2078 | P | YVGL PROTEIN. |
| | ID2079 | P | SULFITE REDUCTASE (NADPH) FLAVOPROTEIN (EC 1.8.1.2). |
| | ID2080 | P | HYPOTHETICAL 21.7 KDA PROTEIN. |
| 40 | ID2081 | P | HYPOTHETICAL PROTEIN YWRB. |
| | ID2082 | P | ORF starting with ATG of length 1458 |
| | ID2083 | P | HYPOTHETICAL 49.9 KDA PROTEIN. |
| | ID2084 | P | HYPOTHETICAL 43.2 KDA PROTEIN IN DNAC-RPLI INTERGENIC |
| | REGION | | |
| 45 | ID2085 | P | PEROXIDE OPERON REGULATOR. |
| | ID2086 | P | HYPOTHETICAL 57.2 KDA PROTEIN. |
| | ID2087 | P | YFIY PROTEIN. |
| | ID2088 | P | PUTATIVE ALKALINE PHOSPHATASE. |
| | ID2089 | P | HYPOTHETICAL PROTEIN YWRA. |
| 50 | ID2090 | P | YVGW PROTEIN. |
| | ID2091 | P | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGH. |
| | ID2092 | P | ARSENIC EFFLUX PUMP. |
| | ID2093 | P | YVGQ (FRAGMENT). |
| | ID2094 | P | YJBD PROTEIN. |
| 55 | ID2095 | P | POTASSIUM CHANNEL PROTEIN. |
| | ID2096 | P | A formate transport associated protein, FTAP2. |
| | ID2097 | P | BH0467 PROTEIN. |
| | ID2098 | P | HYPOTHETICAL 14.6 KDA PROTEIN IN GCVT-SPOIIIAA |
| | INTERGENIC RE | | |
| 60 | ID2099 | P | Vancomycin resistant Enterococcus faecium expression |
| | product | | |
| | ID2100 | P | PROBABLE ABC TRANSPORTER BINDING PROTEIN YXEB |
| | PRECURSOR. | | |
| | ID2101 | P | YOJM PROTEIN. |
| 65 | ID2102 | P | YUSI PROTEIN. |
| | ID2103 | P | HYDROPHOBIC MEMBRANE PROTEIN ZURM. |

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| | ID2104 | P | GENERAL STRESS PROTEIN 80 (GSP80). |
| | ID2105 | P | ORF starting with ATG of length 957 |
| | ID2106 | P | ORF starting with ATG of length 954 |
| | ID2107 | P | YVGQ (FRAGMENT). |
| 5 | ID2108 | P | MODB PROTEIN. |
| | ID2109 | P | ORF starting with ATG of length 933 |
| | ID2110 | P | S. pneumoniae phosphate transport ATP-binding |
| | protein. | | |
| 10 | ID2111 | P | B. subtilis hydrolase protein YJCH. |
| | ID2112 | P | GENERAL STRESS PROTEIN 80 (GSP80). |
| | ID2113 | P | NA+/H ⁺ ANTIPORTER SUBUNIT. |
| | ID2114 | P | HYPOTHETICAL 12.1 KDA PROTEIN IN SACB-CLPP INTERGENIC |
| | REGION | | |
| 15 | ID2115 | P | HYPOTHETICAL 11.4 KDA PROTEIN IN SACB-CLPP INTERGENIC |
| | REGION | | |
| | ID2116 | P | SA0928 PROTEIN. |
| | ID2117 | P | RPOH (FRAGMENT). |
| | ID2118 | P | ORF starting with ATG of length 799 |
| | ID2119 | P | YJBE PROTEIN. |
| 20 | ID2120 | P | HYPOTHETICAL 11.3 KDA PROTEIN IN HMP-PROB INTERGENIC |
| | REGION. | | |
| | ID2121 | P | FEOB PROTEIN. |
| | ID2122 | P | ORF starting with ATG of length 771 |
| | ID2123 | P | TRANSPORTER (PHO87 FAMILY). |
| 25 | ID2124 | P | PEROXIDE OPERON REGULATOR. |
| | ID2125 | P | PUTATIVE ALKALINE PHOSPHATASE. |
| | ID2126 | P | HYPOTHETICAL 11.9 KDA PROTEIN IN HMP-PROB INTERGENIC |
| | REGION. | | |
| 30 | ID2127 | P | MULTIDRUG RESISTANCE PROTEIN EBRB. |
| | ID2128 | P | PEROXIDE OPERON REGULATOR. |
| | ID2129 | P | ORF starting with ATG of length 1005 |
| | ID2130 | P | NA+/H ⁺ ANTIPORTER SUBUNIT. |
| | ID2131 | P | NA+/H ⁺ ANTIPORTER SUBUNIT. |
| | ID2132 | P | YBCF PROTEIN. |
| 35 | ID2133 | P | NITRATE EXTRUSION PROTEIN (FRAGMENT). |
| | ID2134 | P | ORF starting with ATG of length 624 |
| | ID2135 | P | ORF starting with ATG of length 594 |
| | ID2136 | P | YDFA PROTEIN. |
| | ID2137 | P | YTWF PROTEIN. |
| 40 | ID2138 | P | NA+/H ⁺ ANTIPORTER SUBUNIT. |
| | ID2139 | P | CATION-EFFLUX SYSTEM MEMBRANE PROTEIN HOMOLOG. |
| | ID2140 | P | YFLS PROTEIN. |
| | ID2141 | P | B. subtilis hydrolase protein YJCH. |
| | ID2142 | P | HYPOTHETICAL 7.2 KDA PROTEIN. |
| 45 | ID2143 | P | IRON UPTAKE REGULATORY PROTEIN. |
| | ID2144 | P | ABC-TYPE TRANSPORTER, PUTATIVE ATP-BINDING COMPONENT. |
| | ID2145 | P | ORF starting with ATG of length 244 |
| | ID2146 | P | PROBABLE MANGANESE TRANSPORT PROTEIN MNTH. |
| | ID2147 | P | HYPOTHETICAL PROTEIN YWRB. |
| 50 | ID2148 | PH | IRON-UPTAKE SYSTEM PERMEASE PROTEIN FEUB. |
| | ID2149 | PH | HOMOLOGUE OF FERRIC ANGUILIBACTIN TRANSPORT SYSTEM |
| | PERMERASE P | | |
| | ID2150 | PH | YUSV PROTEIN. |
| | ID2151 | PH | YFHA PROTEIN. |
| 55 | ID2152 | PH | IRON-UPTAKE SYSTEM PERMEASE PROTEIN FEUC. |
| | ID2153 | PH | FERRICHROME TRANSPORT SYSTEM PERMEASE PROTEIN FHUG. |
| | ID2154 | PH | FERRICHROME TRANSPORT ATP-BINDING PROTEIN FHUC. |
| | ID2155 | PH | YVRA PROTEIN. |
| | ID2156 | PH | YFMD PROTEIN. |
| 60 | ID2157 | PH | ENTEROCHELIN UPTAKE PERMEASE. |
| | ID2158 | PH | YFME PROTEIN. |
| | ID2159 | PH | PERMEASE PROTEIN OF ABC TRANSPORTER. |
| | ID2160 | PH | FERRICHROME TRANSPORT PERMEASE. |
| | ID2161 | PH | BIRII, ATR, FBID & FBIC GENES (FRAGMENT). |
| 65 | ID2162 | PH | HOMOLOGUE OF IRON DICITRATE TRANSPORT ATP-BINDING |
| | PROTEIN FE | | |

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| | ID2163 | PH | HMUV. |
| | ID2164 | PH | FERRICHROME TRANSPORT SYSTEM PERMEASE PROTEIN FHUB. |
| | ID2165 | PR | ASSIMILATORY NITRITE REDUCTASE [NAD(P)H] SMALL |
| 5 | SUBUNIT (EC 1 | | |
| | ID2166 | Q | LCHAB PROTEIN. |
| | ID2167 | Q | LICHENYSIN SYNTHETASE A. |
| | ID2168 | Q | LICHENYSIN SYNTHETASE A. |
| | ID2169 | Q | ORF starting with ATG of length 8268 |
| | ID2170 | Q | YERP PROTEIN. |
| 10 | ID2171 | Q | ORF starting with ATG of length 7158 |
| | ID2172 | Q | YKNV PROTEIN. |
| | ID2173 | Q | 2,3-DIHYDROXYBENZOATE-AMP LIGASE (EC 6.3.2.-) |
| | (DIHYDROXYBENZ | | |
| | ID2174 | Q | TRANSPORT ATP-BINDING PROTEIN CYDC. |
| 15 | ID2175 | Q | ORF starting with ATG of length 3798 |
| | ID2176 | Q | UNIDENTIFIED TRANSPORTER-ATP BINDING. |
| | ID2177 | Q | HYPOTHETICAL 65.1 KDA PROTEIN. |
| | ID2178 | Q | REGULATORY PROTEIN (FRAGMENT). |
| | ID2179 | Q | HYPOTHETICAL 48.5 KDA PROTEIN IN ILVA 3'REGION. |
| 20 | ID2180 | Q | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN |
| | ACDA 5'R | | |
| | ID2181 | Q | PUTATIVE CYTOCHROME P450 CYPX (EC 1.14.-.-). |
| | ID2182 | Q | CYTOCHROME P450 109 (EC 1.14.-.-) (ORF405). |
| | ID2183 | Q | ATP-BINDING CASSETTE TRANSPORTER A. |
| 25 | ID2184 | Q | NYSH. |
| | ID2185 | Q | "BIOTIN BIOSYNTHESIS; CYTOCHROME P450-LIKE ENZYME (EC |
| | 1.14.-.-" | | |
| | ID2186 | Q | BH2620 PROTEIN. |
| | ID2187 | Q | LANTIBIOTIC MERSACIDIN TRANSPORTER SYSTEM. |
| 30 | ID2188 | Q | YKNX PROTEIN. |
| | ID2189 | Q | HYPOTHETICAL 76.3 KDA PROTEIN. |
| | ID2190 | Q | PUTATIVE CYTOCHROME P450 YJIB (EC 1.14.-.-). |
| | ID2191 | Q | LANTIBIOTIC MERSACIDIN TRANSPORTER SYSTEM. |
| | ID2192 | Q | HYPOTHETICAL 33.7 KDA PROTEIN. |
| 35 | ID2193 | Q | ORF starting with ATG of length 3798 |
| | ID2194 | Q | ORF starting with ATG of length 1950 |
| | ID2195 | Q | TRANSPORT ATP-BINDING PROTEIN CYDD. |
| | ID2196 | Q | PUTATIVE CHALCONE SYNTHASE (EC 2.3.1.74) (NARINGENIN- |
| | CHALCON | | |
| 40 | ID2197 | Q | ALPHA-ACETOLACTATE DECARBOXYLASE (EC 4.1.1.5). |
| | ID2198 | Q | ORF starting with ATG of length 1824 |
| | ID2199 | Q | S. xylosus DltA protein. |
| | ID2200 | Q | DNA-DAMAGE-INDUCIBLE PROTEIN. |
| | ID2201 | Q | ORF starting with ATG of length 1677 |
| 45 | ID2202 | Q | YLPC PROTEIN. |
| | ID2203 | Q | YUEJ PROTEIN. |
| | ID2204 | Q | ORF starting with ATG of length 1470 |
| | ID2205 | Q | ISOCHORISMATASE (EC 3.3.2.1) (2,3 DIHYDRO-2,3 |
| | DIHYDROXYBENZO | | |
| 50 | ID2206 | Q | 4'-PHOSPHOPANTETHENYL TRANSFERASE (EC 2.-.-.-) |
| | (SURFACTIN S | | |
| | ID2207 | Q | HYPOTHETICAL 20.8 KDA PROTEIN IN SERS-DNAZ INTERGENIC |
| | REGION | | |
| | ID2208 | Q | BACITRACIN SYNTHETASE 3 (BA3) (FRAGMENT). |
| 55 | ID2209 | Q | SURFACTIN SYNTHETASE (FRAGMENT). |
| | ID2210 | Q | TRANSPORT ATP-BINDING PROTEIN CYDD. |
| | ID2211 | Q | ABC TRANSPORTER ECSA HOMOLOG. |
| | ID2212 | Q | PUTATIVE ABC TRANSPORTER SUBUNIT EPIF. |
| | ID2213 | Q | 4-OXALOCROTONATE DECARBOXYLASE-LIKE PROTEIN. |
| 60 | ID2214 | Q | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN |
| | GLPD-C | | |
| | ID2215 | Q | YHAQ. |
| | ID2216 | Q | ORF starting with ATG of length 927 |
| | ID2217 | Q | ORF starting with ATG of length 927 |
| 65 | ID2218 | Q | HYPOTHETICAL 50.0 KDA PROTEIN. |
| | ID2219 | Q | ORF starting with ATG of length 885 |

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| | ID2220 | Q | LCHA-TE PROTEIN. |
| | ID2221 | Q | YHBJ PROTEIN. |
| | ID2222 | Q | 308AA LONG HYPOTHETICAL ATP-BINDING TRANSPORT PROTEIN. |
| 5 | ID2223 | Q | ORF starting with ATG of length 852 |
| | ID2224 | Q | ORF starting with ATG of length 885 |
| | ID2225 | Q | ORF starting with ATG of length 834 |
| | ID2226 | Q | HYPOTHETICAL 76.3 KDA PROTEIN. |
| | ID2227 | Q | ATP BINDING PROTEIN BVIA. |
| 10 | ID2228 | Q | YOJI PROTEIN. |
| | ID2229 | Q | ORF starting with ATG of length 780 |
| | ID2230 | Q | ORF starting with ATG of length 759 |
| | ID2231 | Q | ORF starting with ATG of length 690 |
| | ID2232 | Q | CYTOCHROME P450 97B3 (EC 1.14.-.-). |
| 15 | ID2233 | Q | ISOCHORISMATASE (EC 3.3.2.1) (2,3 DIHYDRO-2,3 DIHYDROXYBENZO |
| | ID2234 | Q | ORF starting with ATG of length 636 |
| | ID2235 | Q | HYPOTHETICAL 34.4 KDA PROTEIN. |
| | ID2236 | Q | SA1655 PROTEIN. |
| 20 | ID2237 | Q | HYPOTHETICAL 14.8 KDA PROTEIN. |
| | ID2238 | Q | ISOCHORISMATASE (EC 3.3.2.1) (2,3 DIHYDRO-2,3 DIHYDROXYBENZO |
| | ID2239 | Q | ORF starting with ATG of length 489 |
| | ID2240 | Q | DNA-DAMAGE-INDUCIBLE PROTEIN. |
| 25 | ID2241 | Q | YHBJ PROTEIN. |
| | ID2242 | Q | PUTATIVE CYTOCHROME P450 YJIB (EC 1.14.-.-). |
| | ID2243 | Q | HYPOTHETICAL 30.2 KDA PROTEIN. |
| | ID2244 | Q | ACETYL XYLAN ESTERASE. |
| 30 | ID2245 | Q | ORF starting with ATG of length 354 |
| | ID2246 | Q | ORF starting with ATG of length 353 |
| | ID2247 | Q | BH2936 PROTEIN. |
| | ID2248 | Q | Synthetic ferulic acid decarboxylase clone pGS97b1. |
| | ID2249 | Q | ORF starting with ATG of length 204 |
| | ID2250 | QR | HYPOTHETICAL OXIDOREDUCTASE IN APRE-COMK INTERGENIC REGION (E |
| 35 | ID2251 | QR | YVAG PROTEIN. |
| | ID2252 | QR | HYPOTHETICAL OXIDOREDUCTASE IN RTP-PELB INTERGENIC REGION (E |
| | ID2253 | QR | D-MANNONATE OXIDOREDUCTASE. |
| 40 | ID2254 | QR | H. ghilianii/B. megaterium fusion protein |
| | Tridegin/GlcDH. | | |
| | ID2255 | QR | 3-KETOACYL-ACP REDUCTASE. |
| | ID2256 | QR | 2,3-DIHYDRO-2,3-DIHYDROXYBENZOATE DEHYDROGENASE (EC 1.3.1.28 |
| 45 | ID2257 | QR | YUED PROTEIN. |
| | ID2258 | QR | HYPOTHETICAL 28.3 KDA PROTEIN IN AROD-COMER INTERGENIC REGION |
| | ID2259 | QR | SORBITOL-6-PHOSPHATE DEHYDROGENASE. |
| | ID2260 | QR | ACETOIN(DIACETYL) REDUCTASE. |
| 50 | ID2261 | QR | AT1G54870/F14C21_16. |
| | ID2262 | QR | YTQB. |
| | ID2263 | QR | YRRT PROTEIN. |
| | ID2264 | QR | UNIDENTIFIED DEHYDROGENASE. |
| | ID2265 | QR | GLUCOSE AND RIBITOL DEHYDROGENASE HOMOLOG (FRAGMENT). |
| 55 | ID2266 | QR | B. subtilis hydrolase protein YODH. |
| | ID2267 | QR | YVAG PROTEIN. |
| | ID2268 | QR | YRRM PROTEIN. |
| | ID2269 | QR | PUTATIVE OXIDOREDUCTASE TM0019 (EC 1.-.-.-). |
| | ID2270 | QR | HYPOTHETICAL 31.5 KDA PROTEIN IN KATB 3'REGION. |
| 60 | ID2271 | QR | Amino acid sequence of a beta-ketoacyl-ACP reductase protein |
| | ID2272 | QR | HYPOTHETICAL OXIDOREDUCTASE F53C11.3 (EC 1.-.-.-). |
| | ID2273 | QR | YVAG PROTEIN. |
| | ID2274 | QR | SHORT-CHAIN ALCOHOL DEHYDROGENASE. |
| 65 | ID2275 | QR | 282AA LONG HYPOTHETICAL DEHYDROGENASE. |

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| | ID2276 REGION | QR | HYPOTHETICAL 28.3 KDA PROTEIN IN XPAC-ABRB INTERGENIC |
| | ID2277 | QR | YMF1 PROTEIN. |
| | ID2278 | QR | MLL3372 PROTEIN. |
| 5 | ID2279 | QR | ORF starting with ATG of length 765 |
| | ID2280 | QR | 3-OXOACYL- [ACYL-CARRIER-PROTEIN] REDUCTASE. |
| | ID2281 | QR | PUTATIVE OXIDOREDUCTASE HI0048 (EC 1.---.---). |
| | ID2282 | QR | ORF starting with ATG of length 597 |
| | ID2283 | QR | GRA-ORF6 PROTEIN. |
| 10 | ID2284 | QR | ORF starting with ATG of length 534 |
| | ID2285 REGION | QR | HYPOTHETICAL 19.0 KDA PROTEIN IN ILVD-THYB INTERGENIC |
| | ID2286 | QR | ORF starting with ATG of length 432 |
| | ID2287 | QR | ORF starting with TTG or GTG of length 468 |
| 15 | ID2288 1.2.1.2) (| R | PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT (EC |
| | ID2289 REGION | R | HYPOTHETICAL 74.3 KDA PROTEIN IN RPLI-COTF INTERGENIC |
| 20 | ID2290 REGION | R | HYPOTHETICAL 79.2 KDA PROTEIN IN PHOH-DGKA INTERGENIC |
| | ID2291 REGION | R | HYPOTHETICAL 61.5 KDA PROTEIN IN ADEC-PDHA INTERGENIC |
| | ID2292 | R | YTSD. |
| | ID2293 | R | YFMR. |
| 25 | ID2294 REGION | R | HYPOTHETICAL 78.8 KDA PROTEIN IN TETB-EXOA INTERGENIC |
| | ID2295 REGION | R | HYPOTHETICAL 60.2 KDA PROTEIN IN CSPB-GLPP INTERGENIC |
| | ID2296 | R | YFMM PROTEIN. |
| 30 | ID2297 | R | FORMATE DEHYDROGENASE ALPHA SUBUNIT HOMOLOG. |
| | ID2298 | R | YURU PROTEIN. |
| | ID2299 | R | PROBABLE GTP-BINDING PROTEIN ENGA. |
| | ID2300 | R | HYPOTHETICAL 70.5 KDA PROTEIN IN IDH 3'REGION. |
| | ID2301 | R | SPOOB-ASSOCIATED GTP-BINDING PROTEIN. |
| 35 | ID2302 | R | YURX PROTEIN. |
| | ID2303 | R | BH0531 PROTEIN. |
| | ID2304 REGION | R | HYPOTHETICAL 56.1 KDA PROTEIN IN MFD-DIVIC INTERGENIC |
| | ID2305 | R | ORF11. |
| 40 | ID2306 | R | COME OPERON PROTEIN 3. |
| | ID2307 | R | HYPOTHETICAL HELICASE IN PONA-COTD INTERGENIC REGION. |
| | ID2308 | R | PBSX PHAGE TERMINASE LARGE SUBUNIT. |
| | ID2309 | R | YKPA PROTEIN. |
| | ID2310 45 REGION | R | HYPOTHETICAL 51.2 KDA PROTEIN IN RECO-CMK INTERGENIC |
| | ID2311 | R | YKUU PROTEIN. |
| | ID2312 | R | HYPOTHETICAL 48.9 KDA PROTEIN. |
| | ID2313 | R | MMGE PROTEIN. |
| | ID2314 | R | HYPOTHETICAL 40.1 KDA GTP-BINDING PROTEIN IN RPSF- |
| 50 | SPO0J INTE | R | ORF11. |
| | ID2315 | R | HYPOTHETICAL 50.9 KDA PROTEIN IN SPOIIIC-CWLA |
| | ID2316 INTERGENIC REG | R | POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN. |
| | ID2317 | R | Bacillus subtilis inositol dehydrogenase. |
| 55 | ID2318 | R | ORNITHINE ACETYLTRANSFERASE. |
| | ID2319 | R | HYPOTHETICAL 40.9 KDA PROTEIN IN MECB-GLTX INTERGENIC |
| | ID2320 REGION | R | HYPOTHETICAL 43.6 KDA PROTEIN IN GBSA-TLPB INTERGENIC |
| 60 | ID2321 REGION | R | HYPOTHETICAL 50.0 KDA PROTEIN IN SODA-COMGA |
| | ID2322 INTERGENIC REGIO | R | HYPOTHETICAL 40.7 KDA PROTEIN IN MECB-GLTX INTERGENIC |
| 65 | ID2323 REGION | R | HYPOTHETICAL 48.3 KDA PROTEIN IN QCRA-AROE INTERGENIC |

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| | ID2325 | R | YTQA. |
| | ID2326 | R | YESM PROTEIN. |
| | ID2327 | R | HYPOTHETICAL SYMPORTER YHCL. |
| | ID2328 | R | HYPOTHETICAL 41.0 KDA PROTEIN IN NUCB-AROD INTERGENIC |
| 5 | REGION | | |
| | ID2329 | R | YMFA PROTEIN. |
| | ID2330 | R | HYPOTHETICAL 42.1 KDA PROTEIN IN MOAD-FRUR INTERGENIC |
| | REGION | | |
| 10 | ID2331 | R | ORF starting with ATG of length 2879 |
| | ID2332 | R | HYPOTHETICAL 51.5 KDA PROTEIN IN CITA-SSPB INTERGENIC |
| | REGION | | |
| | ID2333 | R | HYPOTHETICAL 57.4 KDA PROTEIN IN MFD-DIVIC INTERGENIC |
| | REGION | | |
| 15 | ID2334 | R | BH0889 PROTEIN. |
| | ID2335 | R | GTP-BINDING PROTEIN ERA HOMOLOG (BEX PROTEIN). |
| | ID2336 | R | YTRF. |
| | ID2337 | R | AMINOPEPTIDASE. |
| | ID2338 | R | HYPOTHETICAL 51.0 KDA PROTEIN IN PTA 3'REGION. |
| | ID2339 | R | HYPOTHETICAL 37.1 KDA PROTEIN IN FOLK-LYSS INTERGENIC |
| 20 | REGION | | |
| | ID2340 | R | HYPOTHETICAL OXIDOREDUCTASE IN FHUD-OPUBD INTERGENIC |
| | REGION. | | |
| | ID2341 | R | HYPOTHETICAL 33.6 KDA PROTEIN IN TDK-PRFA INTERGENIC |
| | REGION. | | |
| 25 | ID2342 | R | YDFJ PROTEIN. |
| | ID2343 | R | HYPOTHETICAL 37.5 KDA PROTEIN IN DEGA-NPRB INTERGENIC |
| | REGION | | |
| | ID2344 | R | YHAA PROTEIN. |
| | ID2345 | R | YBFQ PROTEIN. |
| 30 | ID2346 | R | YLOQ PROTEIN. |
| | ID2347 | R | PUTATIVE SODIUM-DEPENDENT INNER MEMBRANE TRANSPORT |
| | PROTEIN. | | |
| | ID2348 | R | HOMOLOGUE OF HYPOTHETICAL PROTEIN IN A RAPAMYCIN |
| | SYNTHESIS G | | |
| 35 | ID2349 | R | BH2362 PROTEIN. |
| | ID2350 | R | HYPOTHETICAL 32.9 KDA PROTEIN IN GCVT-SPOIIIAA |
| | INTERGENIC RE | | |
| | ID2351 | R | HYPOTHETICAL 29.5 KDA PROTEIN. |
| | ID2352 | R | YEBB PROTEIN. |
| 40 | ID2353 | R | 2-NITROPROPANE DIOXYGENASE. |
| | ID2354 | R | ORF starting with ATG of length 2250 |
| | ID2355 | R | YKOQ. |
| | ID2356 | R | YTQI. |
| | ID2357 | R | HYPOTHETICAL 30.2 KDA PROTEIN IN IDH-DEOR INTERGENIC |
| 45 | REGION. | | |
| | ID2358 | R | YTNP. |
| | ID2359 | R | SIMILAR TO BACILLUS SUBTILIS YXEH AND YCSE PROTEINS |
| | AND TO E | | |
| | ID2360 | R | PUTATIVE MORPHINE DEHYDROGENASE. |
| 50 | ID2361 | R | HYPOTHETICAL 20.0 KDA PROTEIN IN RRNG-FEUC INTERGENIC |
| | REGION | | |
| | ID2362 | R | ORF starting with ATG of length 2055 |
| | ID2363 | R | YHAA PROTEIN. |
| | ID2364 | R | HYPOTHETICAL 34.5 KDA PROTEIN IN GLTP-CWLJ INTERGENIC |
| 55 | REGION | | |
| | ID2365 | R | YTIP. |
| | ID2366 | R | YRRL PROTEIN. |
| | ID2367 | R | BH2393 PROTEIN. |
| | ID2368 | R | NUCLEOTIDE BINDING PROTEIN EXPZ. |
| 60 | ID2369 | R | YTFP (YTFP PROTEIN). |
| | ID2370 | R | HYPOTHETICAL 33.9 KDA PROTEIN IN LIPB-SSPK INTERGENIC |
| | REGION | | |
| | ID2371 | R | HYPOTHETICAL 24.7 KDA PROTEIN. |
| | ID2372 | R | YQZB PROTEIN. |
| 65 | ID2373 | R | HOMOLOGUES TO NITRILE HYDRATASE REGION 3'- |
| | HYPOTHETICAL PROTE | | |

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| | ID2374 | R | HOMOLOGUE OF HYPOTHETICAL PROTEIN IN A RAPAMYCIN |
| | SYNTHESIS G | | |
| | ID2375 | R | YVGN PROTEIN. |
| 5 | ID2376 | R | HYPOTHETICAL 39.3 KDA PROTEIN. |
| | ID2377 | R | HYPOTHETICAL 32.7 KDA PROTEIN IN FEUA-SIGW INTERGENIC |
| | REGION | | |
| | ID2378 | R | HYPOTHETICAL 24.1 KDA PROTEIN YDIH. |
| | ID2379 | R | PUTATIVE TRANSPORTER. |
| 10 | ID2380 | R | PCRB PROTEIN HOMOLOG. |
| | ID2381 | R | YOJE PROTEIN. |
| | ID2382 | R | HYPOTHETICAL 24.7 KDA PROTEIN IN CSPB-GLPP INTERGENIC |
| | REGION | | |
| | ID2383 | R | YUSB PROTEIN. |
| 15 | ID2384 | R | HYPOTHETICAL ZINC PROTEASE YMKG (EC 3.4.99.-) (ORFP). |
| | ID2385 | R | YCCF PROTEIN. |
| | ID2386 | R | YMFH PROTEIN. |
| | ID2387 | R | YTMQ. |
| | ID2388 | R | HEMOLYSIN III HOMOLOG. |
| | ID2389 | R | TUAB PROTEIN. |
| 20 | ID2390 | R | HYPOTHETICAL 31.5 KDA PROTEIN IN GLVBC 3'REGION. |
| | ID2391 | R | YFNB. |
| | ID2392 | R | YFHG PROTEIN. |
| | ID2393 | R | BH1896 PROTEIN. |
| 25 | ID2394 | R | <i>Bacillus subtilis</i> yihA family member polypeptide |
| | sequence. | | |
| | ID2395 | R | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA |
| | REGION, | | |
| | ID2396 | R | YKVM PROTEIN. |
| 30 | ID2397 | R | HPR (SER-P) PHOSPHATASE (YVOE PROTEIN). |
| | ID2398 | R | YFLN PROTEIN. |
| | ID2399 | R | YUNE PROTEIN. |
| | ID2400 | R | HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC |
| | REGION (E | | |
| | ID2401 | R | HYPOTHETICAL 28.9 KDA PROTEIN. |
| 35 | ID2402 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN |
| | IDH 3' RE | | |
| | ID2403 | R | ORF starting with ATG of length 1722 |
| | ID2404 | R | ABC TRANSPORTER ATP-BINDING PROTEIN HOMOLOGUE. |
| | ID2405 | R | YKVJ PROTEIN. |
| 40 | ID2406 | R | YOAZ. |
| | ID2407 | R | YCZE PROTEIN. |
| | ID2408 | R | HYPOTHETICAL 23.7 KDA PROTEIN IN CCCA-SODA INTERGENIC |
| | REGION | | |
| | ID2409 | R | <i>Bacillus subtilis</i> serine protease SP3 (YITV). |
| 45 | ID2410 | R | HYPOTHETICAL 19.0 KDA PROTEIN IN GLPD-CSPB INTERGENIC |
| | REGION | | |
| | ID2411 | R | UNKNOWN (BH2089 PROTEIN). |
| | ID2412 | R | HYPOTHETICAL 35.9 KDA PROTEIN. |
| 50 | ID2413 | R | YRRB PROTEIN. |
| | ID2414 | R | HYPOTHETICAL 37.5 KDA PROTEIN YDHJ. |
| | ID2415 | R | HYPOTHETICAL 30.6 KDA PROTEIN. |
| | ID2416 | R | ORF starting with ATG of length 1584 |
| | ID2417 | R | RECOMBINATION PROTEIN U (PENICILLIN-BINDING PROTEIN- |
| | RELATED | | |
| 55 | ID2418 | R | PUTATIVE ACETYLTRANSFERASE. |
| | ID2419 | R | HYPOTHETICAL 27.6 KDA PROTEIN IN BLTR-SPOIIC |
| | INTERGENIC REG | | |
| | ID2420 | R | PUTATIVE BETA-PHOSPHOGLUCOMUTASE (EC 5.4.2.6) (BETA- |
| | PGM). | | |
| 60 | ID2421 | R | YTSC PROTEIN. |
| | ID2422 | R | HOMOLOGUE OF UNIDENTIFIED PROTEIN OF E. COLI. |
| | ID2423 | R | HYPOTHETICAL 32.9 KDA PROTEIN IN BLTR-SPOIIC |
| | INTERGENIC REG | | |
| | ID2424 | R | FUNCTION UNKNOWN. |
| 65 | ID2425 | R | BH1010 PROTEIN. |
| | ID2426 | R | HYPOTHETICAL 33.2 KDA PROTEIN. |

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| | ID2427 | R | HYPOTHETICAL 19.7 KDA PROTEIN IN CYSS 3' REGION. |
| | ID2428 | R | HYPOTHETICAL 137.4 KDA PROTEIN IN BCSA-DEGR |
| | INTERGENIC REGIO | | |
| 5 | ID2429 | R | YNGD PROTEIN. |
| | ID2430 | R | HYPOTHETICAL 35.8 KDA PROTEIN IN GLNQ-ANSR INTERGENIC REGION |
| | ID2431 | R | YTDI. |
| | ID2432 | R | YTET. |
| 10 | ID2433 | R | HYPOTHETICAL 24.5 KDA PROTEIN IN NARQ-SPOIID |
| | INTERGENIC REGI | | |
| | ID2434 | R | YKUE PROTEIN. |
| | ID2435 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YDIF. |
| 15 | ID2436 | R | YDCA PROTEIN. |
| | ID2437 | R | BH1564 PROTEIN. |
| | ID2438 | R | HYPOTHETICAL 20.1 KDA PROTEIN IN NUCB-AROD INTERGENIC REGION |
| | ID2439 | R | YTET. |
| 20 | ID2440 | R | YTOA. |
| | ID2441 | R | HYPOTHETICAL 27.9 KDA PROTEIN. |
| | ID2442 | R | ORF starting with ATG of length 1419 |
| | ID2443 | R | HYPOTHETICAL 41.6 KDA PROTEIN IN FMT-SPOVM INTERGENIC REGION |
| 25 | ID2444 | R | ORF starting with ATG of length 1413 |
| | ID2445 | R | GENERAL STRESS PROTEIN 18 (GSP18). |
| | ID2446 | R | CINA-LIKE PROTEIN. |
| | ID2447 | R | HYPOTHETICAL 49.5 KDA PROTEIN IN TGL-PGI INTERGENIC REGION. |
| 30 | ID2448 | R | B. subtilis hydrolase protein YUII. |
| | ID2449 | R | SA0421 PROTEIN. |
| | ID2450 | R | YLOV PROTEIN. |
| | ID2451 | R | YTNM. |
| | ID2452 | R | HYPOTHETICAL 40.6 KDA PROTEIN IN CITZ-PYKA INTERGENIC REGION |
| 35 | ID2453 | R | MLL7248 PROTEIN. |
| | ID2454 | R | BH3078 PROTEIN. |
| | ID2455 | R | YTPR. |
| | ID2456 | R | YKUL PROTEIN. |
| 40 | ID2457 | R | ACETOIN UTILIZATION ACUB PROTEIN. |
| | ID2458 | R | MALTOSE TRANSACETYLASE (MALTOSE O-ACETYLTRANSFERASE) (EC 2.3) |
| | ID2459 | R | JAG PROTEIN (SPOIIJJ ASSOCIATED PROTEIN). |
| | ID2460 | R | HYPOTHETICAL 22.0 KDA PROTEIN IN RECO-CMK INTERGENIC REGION. |
| 45 | ID2461 | R | HYPOTHETICAL 41.6 KDA PROTEIN IN FMT-SPOVM INTERGENIC REGION |
| | ID2462 | R | BH1956 PROTEIN. |
| | ID2463 | R | BH0846 PROTEIN. |
| | ID2464 | R | COMF OPERON PROTEIN 3. |
| 50 | ID2465 | R | HYPOTHETICAL 56.4 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| | ID2466 | R | LIPOPOLYSACCHARIDE BIOSYNTHESIS PROTEIN BPLA. |
| | ID2467 | R | YUIG PROTEIN. |
| | ID2468 | R | YKNY PROTEIN. |
| 55 | ID2469 | R | BH3002 PROTEIN. |
| | ID2470 | R | HYPOTHETICAL 23.2 KDA PROTEIN. |
| | ID2471 | R | HYPOTHETICAL 22.5 KDA PROTEIN. |
| | ID2472 | R | ORF starting with ATG of length 1233 |
| | ID2473 | R | YFHB PROTEIN. |
| 60 | ID2474 | R | BH2921 PROTEIN. |
| | ID2475 | R | UNKNOWN (BH2089 PROTEIN). |
| | ID2476 | R | HYPOTHETICAL 41.0 KDA PROTEIN. |
| | ID2477 | R | B. subtilis hydrolase protein YCGS. |
| | ID2478 | R | SPORE MATURATION PROTEIN A. |
| 65 | ID2479 | R | YOLF. |
| | ID2480 | R | PUTATIVE - PROBABLE ESTERASE. |

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| | ID2481 | R | HYPOTHETICAL 39.6 KDA PROTEIN IN ALAS-GLNQ INTERGENIC |
| | REGION | | |
| | ID2482 | R | HYPOTHETICAL 34.9 KDA PROTEIN IN GLPD-CSPB INTERGENIC |
| | REGION | | |
| 5 | ID2483 | R | Human secreted protein sequence encoded by gene 4 SEQ |
| | ID NO: | | |
| | ID2484 | R | GALACTOSYLTRANSFERASE-RELATED PROTEIN. |
| | ID2485 | R | HYPOTHETICAL 18.8 KDA PROTEIN IN ECSC-PBPF INTERGENIC |
| | REGION | | |
| 10 | ID2486 | R | HYPOTHETICAL 24.0 KDA PROTEIN IN NARQ-SPOIID |
| | INTERGENIC | REGI | |
| | ID2487 | R | ORF starting with ATG of length 1146 |
| | ID2488 | R | HYPOTHETICAL 41.0 KDA PROTEIN. |
| | ID2489 | R | ORF starting with ATG of length 1134 |
| 15 | ID2490 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN |
| | YDIF. | | |
| | ID2491 | R | YDCJ PROTEIN. |
| | ID2492 | R | HYPOTHETICAL 17.4 KDA PROTEIN. |
| | ID2493 | R | YJBI PROTEIN. |
| 20 | ID2494 | R | HYPOTHETICAL 21.1 KDA PROTEIN. |
| | ID2495 | R | HYPOTHETICAL. |
| | ID2496 | R | HYPOTHETICAL 137.4 KDA PROTEIN IN BCSA-DEGR |
| | INTERGENIC | REGIO | |
| | ID2497 | R | COENZYME PQQ SYNTHESIS PROTEIN (PQQE). |
| 25 | ID2498 | R | HYPOTHETICAL 28.6 KDA PROTEIN IN RECQ-CMK INTERGENIC |
| | REGION | | |
| | ID2499 | R | ORF starting with ATG of length 1056 |
| | ID2500 | R | HYPOTHETICAL 22.8 KDA PROTEIN. |
| | ID2501 | R | HYPOTHETICAL 19.5 KDA PROTEIN. |
| 30 | ID2502 | R | ORF starting with ATG of length 1053 |
| | ID2503 | R | HYPOTHETICAL 14.9 KDA PROTEIN IN CSPB-GLPP INTERGENIC |
| | REGION | | |
| | ID2504 | R | ORF starting with ATG of length 1044 |
| | ID2505 | R | BH2278 PROTEIN. |
| 35 | ID2506 | R | HYPOTHETICAL 49.5 KDA PROTEIN IN TGL-PGI INTERGENIC |
| | REGION. | | |
| | ID2507 | R | ORF starting with ATG of length 1020 |
| | ID2508 | R | PHOSPHOTRIESTERASE HOMOLOGY PROTEIN. |
| | ID2509 | R | ACYLTRANSFERASE, PUTATIVE. |
| 40 | ID2510 | R | INTRACELLULAR PROTEINASE. |
| | ID2511 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2512 | R | YLOV PROTEIN. |
| | ID2513 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN |
| | YDIF. | | |
| 45 | ID2514 | R | VEGETATIVE PROTEIN 296 (VEG296). |
| | ID2515 | R | BH2279 PROTEIN. |
| | ID2516 | R | HYPOTHETICAL 49.0 KDA PROTEIN IN BLTD-TRKA INTERGENIC |
| | REGION | | |
| | ID2517 | R | HYPOTHETICAL 23.1 KDA PROTEIN IN BSAA-ILVD INTERGENIC |
| 50 | REGION | | |
| | ID2518 | R | SA0084 PROTEIN. |
| | ID2519 | R | HYPOTHETICAL 11.3 KDA PROTEIN. |
| | ID2520 | R | HYPOTHETICAL 20.5 KDA PROTEIN. |
| | ID2521 | R | BH1964 PROTEIN. |
| 55 | ID2522 | R | HYPOTHETICAL 21.6 KDA PROTEIN IN ILVA 3'REGION. |
| | ID2523 | R | HYPOTHETICAL PROTEIN NMB0739. |
| | ID2524 | R | HOMOLOGUES TO NITRILE HYDRATASE REGION 3' |
| | HYPOTHETICAL PROTE | | |
| | ID2525 | R | BH2398 PROTEIN. |
| 60 | ID2526 | R | LYASE (OXO-ACID) |
| | ID2527 | R | PROBABLE MEMBRANE SPANNING PROTEIN. |
| | ID2528 | R | HOMOLOGUE OF HYPOTHETICAL PROTEIN IN A RAPAMYCIN |
| | SYNTHESIS G | | |
| | ID2529 | R | ORF starting with ATG of length 879 |
| 65 | ID2530 | R | MDAB PROTEIN HOMOLOG. |
| | ID2531 | R | HYPOTHETICAL 27.7 KDA PROTEIN. |

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| | ID2532 | R | HOMOLOGUE OF UNIDENTIFIED PROTEIN OF E. COLI. |
| | ID2533 | R | YOBT. |
| | ID2534 | R | HYPOTHETICAL 36.5 KDA PROTEIN IN GBSA-TLPB INTERGENIC |
| | REGION | | |
| 5 | ID2535 | R | HYPOTHETICAL 19.2 KDA PROTEIN IN RPH-ILVB INTERGENIC |
| | REGION. | | |
| | ID2536 | R | BH1151 PROTEIN. |
| | ID2537 | R | CHAPERONIN INVOLVED IN PROTEIN SECRETION. |
| | ID2538 | R | YTDI. |
| 10 | ID2539 | R | FORMATE HYDROGENASE. |
| | ID2540 | R | HYPOTHETICAL 30.7 KDA PROTEIN. |
| | ID2541 | R | LACTAM UTILIZATION PROTEIN. |
| | ID2542 | R | ORF starting with ATG of length 783 |
| | ID2543 | R | ORF starting with ATG of length 774 |
| 15 | ID2544 | R | ABC TRANSPORTER, ATP BINDING PROTEIN. |
| | ID2545 | R | YTGP. |
| | ID2546 | R | B. subtilis nitroreductase Bs YrwO. |
| | ID2547 | R | HYPOTHETICAL 13.0 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| 20 | ID2548 | R | YDFJ PROTEIN. |
| | ID2549 | R | ORF starting with ATG of length 756 |
| | ID2550 | R | YDFE PROTEIN. |
| | ID2551 | R | BH0392 PROTEIN. |
| | ID2552 | R | HYPOTHETICAL 32.6 KDA PROTEIN. |
| 25 | ID2553 | R | SA2112 PROTEIN. |
| | ID2554 | R | HYPOTHETICAL 28.6 KDA PROTEIN IN RECQ-CMK INTERGENIC |
| | REGION | | |
| | ID2555 | R | DLTE PROTEIN. |
| | ID2556 | R | INTRACELLULAR PROTEINASE (EC 3.2.). |
| 30 | ID2557 | R | Bacillus subtilis metalloprotease YhaA. |
| | ID2558 | R | HYPOTHETICAL 39.6 KDA PROTEIN IN ALAS-GLNQ INTERGENIC |
| | REGION | | |
| | ID2559 | R | BH2605 PROTEIN. |
| | ID2560 | R | ORF starting with ATG of length 687 |
| 35 | ID2561 | R | YBBA PROTEIN. |
| | ID2562 | R | HYPOTHETICAL 13.6 KDA PROTEIN. |
| | ID2563 | R | YDDR PROTEIN. |
| | ID2564 | R | YTKL. |
| | ID2565 | R | ORF starting with ATG of length 648 |
| 40 | ID2566 | R | BH2138 PROTEIN. |
| | ID2567 | R | CG1349 PROTEIN. |
| | ID2568 | R | MLL5156 PROTEIN. |
| | ID2569 | R | ORF starting with ATG of length 609 |
| | ID2570 | R | ORF starting with ATG of length 735 |
| 45 | ID2571 | R | COMPETENCE-DAMAGE INDUCIBLE PROTEIN. |
| | ID2572 | R | YFBH PROTEIN. |
| | ID2573 | R | YVAK PROTEIN. |
| | ID2574 | R | YKVM PROTEIN. |
| | ID2575 | R | HYPOTHETICAL 78.8 KDA PROTEIN IN TETB-EXOA INTERGENIC |
| 50 | REGION | | |
| | ID2576 | R | HYPOTHETICAL 9.1 KDA PROTEIN IN TETB-EXOA INTERGENIC |
| | REGION. | | |
| | ID2577 | R | ORF starting with ATG of length 546 |
| | ID2578 | R | YTNM. |
| 55 | ID2579 | R | HYPOTHETICAL HELICASE IN PONA-COTD INTERGENIC REGION. |
| | ID2580 | R | FORMATE HYDROGENASE. |
| | ID2581 | R | HYPOTHETICAL 7.1 KDA PROTEIN. |
| | ID2582 | R | NAD(P)H OXIDOREDUCTASE. |
| | ID2583 | R | ORF starting with ATG of length 2879 |
| 60 | ID2584 | R | BH2906 PROTEIN. |
| | ID2585 | R | ORF starting with ATG of length 480 |
| | ID2586 | R | ORF starting with ATG of length 447 |
| | ID2587 | R | BH2982 PROTEIN. |
| | ID2588 | R | HYPOTHETICAL 23.6 KDA PROTEIN. |
| 65 | ID2589 | R | HYPOTHETICAL PROTEIN VC2101. |
| | ID2590 | R | YFMR. |

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| | ID2591 | R | HYPOTHETICAL 27.6 KDA PROTEIN. |
| | ID2592 | R | ORF starting with ATG of length 408 |
| | ID2593 | R | ORF starting with ATG of length 409 |
| 5 | ID2594 | R | Amino acid sequence of <i>N. meningitidis</i> protein ORF77. |
| | ID2595 | R | CMP-BINDING PROTEIN. |
| | ID2596 | R | BH3997 PROTEIN. |
| | ID2597 | R | PUTATIVE MEMBRANE PROTEIN YDGH. |
| | ID2598 | R | COENZYME PQQ SYNTHESIS PROTEIN (PQQE). |
| | ID2599 | R | BH2605 PROTEIN. |
| 10 | ID2600 | R | ORF starting with TTG or GTG of length 726 |
| | ID2601 | R | ORF starting with ATG of length 354 |
| | ID2602 | R | PUTATIVE BIFUNCTIONAL ENZYME WXCM. |
| | ID2603 | R | ORF starting with ATG of length 348 |
| | ID2604 | R | GENERAL STRESS PROTEIN 14 (GSP14) (EC 1.6.99.-). |
| 15 | ID2605 | R | ORF starting with ATG of length 324 |
| | ID2606 | R | ORF starting with ATG of length 321 |
| | ID2607 | R | HYPOTHETICAL 33.0 KDA PROTEIN IN XPAC-ABRB INTERGENIC REGION |
| | ID2608 | R | PUTATIVE METHIONYL-TRNA SYNTHETASE. |
| 20 | ID2609 | R | F44E7.4 PROTEIN. |
| | ID2610 | R | PUTATIVE TERMINASE LARGE SUBUNIT. |
| | ID2611 | R | ORF starting with ATG of length 270 |
| | ID2612 | R | HYPOTHETICAL 30.8 KDA PROTEIN. |
| | ID2613 | R | BH0590 PROTEIN. |
| 25 | ID2614 | R | YTPR. |
| | ID2615 | R | ORF starting with ATG of length 225 |
| | ID2616 | R | HYPOTHETICAL 32.8 KDA PROTEIN IN BIO3-HXT17 INTERGENIC REGION |
| | ID2617 | R | ORF starting with ATG of length 210 |
| 30 | ID2618 | R | BIOTIN SULFOXIDE REDUCTASE. |
| | ID2619 | R | ORF starting with ATG of length 870 |
| | ID2620 | R | HYPOTHETICAL 79.2 KDA PROTEIN IN PHOH-DGKA INTERGENIC REGION |
| | ID2621 | R | HYPOTHETICAL 74.3 KDA PROTEIN IN RPLI-COTF INTERGENIC REGION |
| 35 | ID2622 | S | ATP-DEPENDENT NUCLEASE SUBUNIT B. |
| | ID2623 | S | YVNB. |
| | ID2624 | S | Enzyme exhibiting activity on arabinan and galactan. |
| Possibl | ID2625 | S | <i>Bacillus licheniformis</i> Pectin lyase III. |
| | ID2626 | S | YFHO PROTEIN. |
| | ID2627 | S | YESX PROTEIN. |
| | ID2628 | S | YETA PROTEIN. |
| | ID2629 | S | HYPOTHETICAL 171.0 KDA PROTEIN IN SPOIIIC-CWLA |
| 45 | INTERGENIC RE | | |
| | ID2630 | S | YDAL PROTEIN. |
| | ID2631 | S | YDAN PROTEIN. |
| | ID2632 | S | ORF starting with ATG of length 4557 |
| | ID2633 | S | STAGE V SPORULATION PROTEIN R. |
| 50 | ID2634 | S | YFIX. |
| | ID2635 | S | BETA-N-ACETYLGLUCOSAMINIDASE PRECURSOR (EC 3.2.1.-). |
| | ID2636 | S | BH1550 PROTEIN. |
| | ID2637 | S | Patent NN No. 5481Arabinogalactan endo-1,4-beta-galactosidas |
| 55 | ID2638 | S | Bacillus licheniformis endo-beta-1,4-glucanase. |
| | ID2639 | S | HYPOTHETICAL 46.0 KDA PROTEIN (TRANSPOSASE OF TN10). |
| | ID2640 | S | Phytase gene from <i>Bacillus licheniformis</i> . Homologous to unkn |
| | ID2641 | S | STAGE IV SPORULATION PROTEIN A. |
| 60 | ID2642 | S | ORF starting with ATG of length 3927 |
| | ID2643 | S | SEPTATION RING FORMATION REGULATOR. |
| | ID2644 | S | LEVANSUCRASE PRECURSOR (EC 2.4.1.10) (BETA-D- |
| | FRUCTOFURANOSYL | | |
| | ID2645 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDE. |
| 65 | ID2646 | S | ORF starting with ATG of length 3519 |
| | ID2647 | S | YKOR. |

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| | ID2648 | S | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA |
| | REGION, | | |
| | ID2649 | S | STAGE V SPORULATION PROTEIN AF. |
| | ID2650 | S | A Bacillus pectate lyase and JP170 alpha-amylase |
| 5 | fusion prot | | |
| | ID2651 | S | HYPOTHETICAL 58.0 KDA PROTEIN IN COTC-LEXA INTERGENIC |
| | REGION | | |
| | ID2652 | S | HYPOTHETICAL ATP:GUANIDO PHOSPHOTRANSFERASE YACI (EC |
| | 2.7.3.- | | |
| 10 | ID2653 | S | YTPB. |
| | ID2654 | S | ORF starting with ATG of length 3222 |
| | ID2655 | S | Family 1 Pectate lyase.29% identical to BioPrep |
| | (SP958).50% | | |
| 15 | ID2656 | S | YBBR PROTEIN. |
| | ID2657 | S | HYPOTHETICAL 48.8 KDA PROTEIN. |
| | ID2658 | S | HYPOTHETICAL 46.0 KDA PROTEIN IN FEUA-SIGW INTERGENIC |
| | REGION | | |
| | ID2659 | S | YESS PROTEIN. |
| 20 | ID2660 | S | ORF starting with ATG of length 3057 |
| | ID2661 | S | YDJI PROTEIN. |
| | ID2662 | S | HYPOTHETICAL 35.6 KDA PROTEIN IN RPSU-PHOH |
| | INTERGENIC REGIO | | |
| | ID2663 | S | 2-KETO-3-DEOXYGLUCONATE PERMEASE (KDG PERMEASE). |
| | ID2664 | S | HYPOTHETICAL 42.6 KDA PROTEIN. |
| 25 | ID2665 | S | C4-DICARBOXYLATE TRANSPORT SYSTEM (PERMEASE LARGE |
| | PROTEIN). | | |
| | ID2666 | S | HYPOTHETICAL 36.3 KDA PROTEIN. |
| | ID2667 | S | STAGE III SPORULATION PROTEIN AE. |
| 30 | ID2668 | S | Xyloglucanase |
| | ID2669 | S | ORF starting with ATG of length 3519 |
| | ID2670 | S | YESR PROTEIN. |
| | ID2671 | S | HYPOTHETICAL 48.6 KDA PROTEIN IN SERS-DNAZ INTERGENIC |
| | REGION | | |
| | ID2672 | S | HYPOTHETICAL 47.4 KDA PROTEIN. |
| 35 | ID2673 | S | PROBABLE HTH_LYSR_FAMILY TRANSCRIPTIONAL REGULATOR. |
| | ID2674 | S | YFHP PROTEIN. |
| | ID2675 | S | YDJG PROTEIN. |
| | ID2676 | S | YNDJ PROTEIN. |
| 40 | ID2677 | S | HYPOTHETICAL 45.3 KDA PROTEIN IN PRKA-CSPB. INTERGENIC |
| | REGION | | |
| | ID2678 | S | YDAJ PROTEIN. |
| | ID2679 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDG. |
| | ID2680 | S | YLBC PROTEIN. |
| | ID2681 | S | SPORE GERMINATION PROTEIN KA. |
| 45 | ID2682 | S | YTER. |
| | ID2683 | S | BH2622 PROTEIN. |
| | ID2684 | S | YKRT PROTEIN. |
| | ID2685 | S | DNA, COMPLETE SEQUENCE. |
| 50 | ID2686 | S | HYPOTHETICAL 43.8 KDA PROTEIN IN XPAC-ABRB INTERGENIC |
| | REGION | | |
| | ID2687 | S | HYPOTHETICAL 37.7 KDA PROTEIN IN RPSF-SPOOJ |
| | INTERGENIC REGIO | | |
| | ID2688 | S | HYPOTHETICAL 34.7 KDA PROTEIN IN CRH-TRXB INTERGENIC |
| | REGION. | | |
| 55 | ID2689 | S | PTS SYSTEM, FRUCTOSE-SPECIFIC IID COMPONENT (EIID- |
| | (FRUC | | |
| | ID2690 | S | PROTEIN ECSB. |
| | ID2691 | S | LANTIBIOTIC MERSACIDIN MODIFYING ENZYME. |
| 60 | ID2692 | S | HYPOTHETICAL 45.0 KDA PROTEIN IN FDRA-ARCC INTERGENIC |
| | REGION | | |
| | ID2693 | S | HYPOTHETICAL 37.0 KDA PROTEIN IN SPOIIIC-CWLA |
| | INTERGENIC REG | | |
| | ID2694 | S | YWSC PROTEIN. |
| | ID2695 | S | HYPOTHETICAL PROTEIN VC1332. |
| 65 | ID2696 | S | YCEH. |
| | ID2697 | S | YLQG PROTEIN. |

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| | ID2698 | S | IOLB PROTEIN. |
| | ID2699 | S | HYPOTHETICAL 43.0 KDA PROTEIN (YVFB PROTEIN). |
| | ID2700 | S | YNDE PROTEIN (PUTATIVE SPORE GERMINATION PROTEIN). |
| | ID2701 | S | HYPOTHETICAL 30.3 KDA PROTEIN IN GLYS-DNAG/DNAE |
| 5 | INTERGENIC R | | |
| | ID2702 | S | HYPOTHETICAL 38.5 KDA PROTEIN IN PONA-COTD INTERGENIC REGION |
| | ID2703 | S | HYPOTHETICAL 41.5 KDA PROTEIN. |
| | ID2704 | S | YJBA PROTEIN. |
| 10 | ID2705 | S | PROTEIN DLTD PRECURSOR. |
| | ID2706 | S | PTS SYSTEM, FRUCTOSE-SPECIFIC IIC COMPONENT (EIIC-FRU) (FRUC |
| | ID2707 | S | HYPOTHETICAL 35.0 KDA PROTEIN IN SPOIIIIC-CWLA |
| | INTERGENIC REG | | |
| 15 | ID2708 | S | GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE. |
| | ID2709 | S | HYPOTHETICAL 34.4 KDA PROTEIN IN RRND 5'REGION. |
| | ID2710 | S | YBCD PROTEIN. |
| | ID2711 | S | HYPOTHETICAL 51.4 KDA PROTEIN. |
| 20 | ID2712 | S | HYPOTHETICAL 32.5 KDA PROTEIN IN CCCA-SODA INTERGENIC REGION |
| | ID2713 | S | YVLB. |
| | ID2714 | S | YLAA PROTEIN. |
| | ID2715 | S | HYPOTHETICAL 41.9 KDA PROTEIN. |
| | ID2716 | S | EXO-POLY-ALPHA-D-GALACTURONOSIDASE, PUTATIVE. |
| 25 | ID2717 | S | SPORULATION SIGMA-E FACTOR PROCESSING PEPTIDASE (EC 3.4.23.-) |
| | ID2718 | S | YUBB PROTEIN. |
| | ID2719 | S | SPORE GERMINATION PROTEIN A2. |
| | ID2720 | S | PUTATIVE SUGAR ISOMERASE. |
| 30 | ID2721 | S | TUAE PROTEIN. |
| | ID2722 | S | HYPOTHETICAL 40.6 KDA PROTEIN. |
| | ID2723 | S | LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR. |
| | ID2724 | S | DIPICOLINATE SYNTHASE, A CHAIN. |
| 35 | ID2725 | S | YKOV PROTEIN. |
| | ID2726 | S | HYPOTHETICAL 36.0 KDA PROTEIN IN GCVT-SPOIIIAA |
| | INTERGENIC RE | | |
| | ID2727 | S | YOAT. |
| | ID2728 | S | HYPOTHETICAL 42.9 KDA PROTEIN. |
| 40 | ID2729 | S | BH2618 PROTEIN. |
| | ID2730 | S | SACPA OPERON ANTITERMINATOR. |
| | ID2731 | S | YFLP PROTEIN. |
| | ID2732 | S | SPORE GERMINATION PROTEIN KB. |
| | ID2733 | S | YFNK. |
| 45 | ID2734 | S | YDCC PROTEIN. |
| | ID2735 | S | YJCL PROTEIN. |
| | ID2736 | S | YVJA. |
| | ID2737 | S | SPORE GERMINATION PROTEIN A1. |
| | ID2738 | S | HYPOTHETICAL 32.2 KDA PROTEIN IN BMRU-ANSR INTERGENIC REGION |
| 50 | ID2739 | S | PUTATIVE SPORE GERMINATION PROTEIN. |
| | ID2740 | S | HYPOTHETICAL 29.6 KDA PROTEIN IN RIBT-DACB INTERGENIC REGION |
| | ID2741 | S | YFKD PROTEIN. |
| 55 | ID2742 | S | HYPOTHETICAL 45.7 KDA PROTEIN IN RPSU-PHOH |
| | INTERGENIC REGIO | | |
| | ID2743 | S | DEGV PROTEIN. |
| | ID2744 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDK. |
| | ID2745 | S | YVOD. |
| 60 | ID2746 | S | YDAH PROTEIN. |
| | ID2747 | S | HYPOTHETICAL 48.2 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| | ID2748 | S | YTAP. |
| | ID2749 | S | RESPONSE REGULATOR ASPARTATE PHOSPHATASE. |
| 65 | ID2750 | S | HYPOTHETICAL 37.3 KDA PROTEIN. |
| | ID2751 | S | YJBH PROTEIN. |

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| | ID2752 | S | LANTIBIOTIC MERSACIDIN MODIFYING ENZYME. |
| | ID2753 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC COMPONENT (SIIBC |
| | ID2754 | S | ORF starting with ATG of length 2089 |
| 5 | ID2755 | S | YOAJ. |
| | ID2756 | S | YITL PROTEIN. |
| | ID2757 | S | EXOGLUCANASE B PRECURSOR (EC 3.2.1.91) (EXOCELLLOBIOHYDROLASE |
| 10 | ID2758 | S | HYPOTHETICAL 28.1 KDA PROTEIN IN SIPU-KIPI INTERGENIC REGION |
| | ID2759 | S | YDEG PROTEIN. |
| | ID2760 | S | YERB PROTEIN. |
| | ID2761 | S | ORF25. |
| 15 | ID2762 | S | HYPOTHETICAL 51.5 KDA PROTEIN. |
| | ID2763 | S | YCEG. |
| | ID2764 | S | HYPOTHETICAL 38.0 KDA PROTEIN IN GIRA-GUAB INTERGENIC REGION |
| | ID2765 | S | ORF starting with ATG of length 1974 |
| 20 | ID2766 | S | SAPB PROTEIN. |
| | ID2767 | S | PUTATIVE SIGMA-B REGULATOR. |
| | ID2768 | S | YQFO PROTEIN. |
| | ID2769 | S | ORF40. |
| | ID2770 | S | YLNE PROTEIN. |
| 25 | ID2771 | S | HYPOTHETICAL 31.2 KDA PROTEIN IN XPAC-ABRB INTERGENIC REGION |
| | ID2772 | S | ORF22. |
| | ID2773 | S | ORF starting with ATG of length 1935 |
| | ID2774 | S | Amino acid sequence of a mature TasA antibiotic protein. |
| 30 | ID2775 | S | PBSX PHAGE TERMINASE SMALL SUBUNIT. |
| | ID2776 | S | BH3947 PROTEIN. |
| | ID2777 | S | HYPOTHETICAL 38.6 KDA PROTEIN IN CYSG-TRPS INTERGENIC REGION |
| | ID2778 | S | YVBY PROTEIN. |
| 35 | ID2779 | S | ORF starting with ATG of length 1896 |
| | ID2780 | S | ORF starting with ATG of length 1860 |
| | ID2781 | S | YFLM PROTEIN. |
| | ID2782 | S | ORF starting with ATG of length 1854 |
| 40 | ID2783 | S | YBCD PROTEIN. |
| | ID2784 | S | Bacillus licheniformis endo-beta-1,4-glucanase. |
| | ID2785 | S | YUTH PROTEIN. |
| | ID2786 | S | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA REGION, |
| 45 | ID2787 | S | HYPOTHETICAL 33.3 KDA PROTEIN IN DNAI-THRS INTERGENIC REGION |
| | ID2788 | S | INTRACELLULAR ALKALINE PROTEASE. |
| | ID2789 | S | SPAЕ. |
| | ID2790 | S | YOJO PROTEIN. |
| 50 | ID2791 | S | HYPOTHETICAL 22.2 KDA PROTEIN IN RECO-CMK INTERGENIC REGION. |
| | ID2792 | S | YUNF PROTEIN. |
| | ID2793 | S | ACETOIN UTILIZATION PROTEIN ACUA (EC 2.3.1.-). |
| | ID2794 | S | SPORE GERMINATION PROTEIN A3 PRECURSOR. |
| 55 | ID2795 | S | HYPOTHETICAL 47.7 KDA PROTEIN IN METS-KSGA INTERGENIC REGION |
| | ID2796 | S | YLBM PROTEIN. |
| | ID2797 | S | HYPOTHETICAL 21.3 KDA PROTEIN. |
| | ID2798 | S | HYPOTHETICAL 25.4 KDA PROTEIN IN DPPE-HMP INTERGENIC REGION. |
| 60 | ID2799 | S | HYPOTHETICAL 28.7 KDA PROTEIN IN GLXK-ALLC INTERGENIC REGION |
| | ID2800 | S | BH2265 PROTEIN. |
| | ID2801 | S | ORF starting with ATG of length 1782 |
| | ID2802 | S | SPOIISA PROTEIN. |
| 65 | ID2803 | S | NECROSIS AND ETHYLENE INDUCING PROTEIN. |
| | ID2804 | S | YLOP PROTEIN. |

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| | ID2805 | S | YLOC PROTEIN. |
| | ID2806 | S | HYPOTHETICAL 40.7 KDA PROTEIN IN FER-RECQ INTERGENIC |
| | REGION. | | |
| 5 | ID2807 | S | HYPOTHETICAL 23.8 KDA PROTEIN. |
| | ID2808 | S | HYPOTHETICAL 25.7 KDA PROTEIN IN BCSA-DEGR INTERGENIC |
| | REGION | | |
| | ID2809 | S | YDEI (BH2088 PROTEIN). |
| | ID2810 | S | ORF38. |
| 10 | ID2811 | S | YJBC PROTEIN. |
| | ID2812 | S | YITD PROTEIN. |
| | ID2813 | S | ORF starting with ATG of length 1725 |
| | ID2814 | S | INNER SPORE COAT PROTEIN H. |
| | ID2815 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDF. |
| | ID2816 | S | ORF13. |
| 15 | ID2817 | S | BH1298 PROTEIN. |
| | ID2818 | S | PROTEIN ECSC. |
| | ID2819 | S | YBDO PROTEIN. |
| | ID2820 | S | PROBABLE PROTEIN ASP-PHOSPHATASE. |
| 20 | ID2821 | S | N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLL PRECURSOR (EC |
| | 3.5.1. | | |
| | ID2822 | S | YDJN PROTEIN. |
| | ID2823 | S | YJBM PROTEIN. |
| | ID2824 | S | HYPOTHETICAL 62.6 KDA PROTEIN IN RPMF-FTSL INTERGENIC |
| | REGION | | |
| 25 | ID2825 | S | YOJO PROTEIN. |
| | ID2826 | S | Bacillus licheniformis Pectate lyase I. |
| | ID2827 | S | HYPOTHETICAL 27.7 KDA PROTEIN IN GPSA-SPOIVA |
| | INTERGENIC REGI | | |
| 30 | ID2828 | S | YKRI PROTEIN. |
| | ID2829 | S | STREPTOGRAMIN B LACTONASE. |
| | ID2830 | S | YDBA PROTEIN. |
| | ID2831 | S | YVQF PROTEIN. |
| | ID2832 | S | BH2292 PROTEIN. |
| 35 | ID2833 | S | YKRX PROTEIN. |
| | ID2834 | S | HYPOTHETICAL 19.5 KDA PROTEIN. |
| | ID2835 | S | HYPOTHETICAL 23.3 KDA PROTEIN. |
| | ID2836 | S | HYPOTHETICAL 51.0 KDA PROTEIN IN TRXB-HISI INTERGENIC |
| | REGION | | |
| 40 | ID2837 | S | TRANSCRIPTION ANTITERMINATOR LICT. |
| | ID2838 | S | SIMILAR TO BACILLUS SUBTILIS YXID PROTEIN. |
| | ID2839 | S | HYPOTHETICAL 27.6 KDA PROTEIN IN FNR-NARG INTERGENIC |
| | REGION. | | |
| | ID2840 | S | STAGE III SPORULATION PROTEIN AA. |
| 45 | ID2841 | S | YJAZ PROTEIN. |
| | ID2842 | S | Bacillus sp. transglutaminase. |
| | ID2843 | S | BH0974 PROTEIN. |
| | ID2844 | S | HYPOTHETICAL 33.3 KDA PROTEIN IN KSGA-VEG INTERGENIC |
| | REGION. | | |
| 50 | ID2845 | S | HYPOTHETICAL 23.4 KDA PROTEIN IN NRDF-CWLC INTERGENIC |
| | REGION | | |
| | ID2846 | S | YVQJ PROTEIN. |
| | ID2847 | S | HYPOTHETICAL 24.8 KDA PROTEIN IN DAPB-PAPS INTERGENIC |
| | REGION | | |
| | ID2848 | S | KINB SIGNALING PATHWAY ACTIVATION PROTEIN. |
| 55 | ID2849 | S | STAGE III SPORULATION PROTEIN AG. |
| | ID2850 | S | YESU PROTEIN. |
| | ID2851 | S | HYPOTHETICAL 22.5 KDA PROTEIN IN RPSF-SPOOJ |
| | INTERGENIC REGIO | | |
| 60 | ID2852 | S | YJAU PROTEIN. |
| | ID2853 | S | YUIC PROTEIN. |
| | ID2854 | S | YDFS PROTEIN. |
| | ID2855 | S | S. pneumoniae derived protein #146. |
| | ID2856 | S | ORF27. |
| 65 | ID2857 | S | YVBJ PROTEIN. |
| | ID2858 | S | HYPOTHETICAL 23.3 KDA PROTEIN. |
| | ID2859 | S | YCDA. |

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| | ID2860 | S | YVGT PROTEIN. |
| | ID2861 | S | BH3996 PROTEIN. |
| | ID2862 | S | YOBG. |
| | ID2863 | S | YTRC. |
| 5 | ID2864 | S | MINOR SPIKE PROTEIN (H PROTEIN) (PILOT PROTEIN). |
| | ID2865 | S | YTEU. |
| | ID2866 | S | HYPOTHETICAL 21.3 KDA PROTEIN IN QCRC-DAPB INTERGENIC |
| | REGION | | |
| | ID2867 | S | RAP60. |
| 10 | ID2868 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDO. |
| | ID2869 | S | YLXX PROTEIN. |
| | ID2870 | S | ORF starting with ATG of length 1491 |
| | ID2871 | S | YKWB PROTEIN. |
| 15 | ID2872 | S | PUTATIVE TRANSCRIPTION REGULATOR. |
| | ID2873 | S | YRVE PROTEIN. |
| | ID2874 | S | SIMILAR TO STAPHYLOCOCCUS AUREUS CAPC PROTEIN. |
| | ID2875 | S | HYPOTHETICAL 30.1 KDA PROTEIN. |
| | ID2876 | S | YUAD PROTEIN. |
| 20 | ID2877 | S | HYPOTHETICAL 21.0 KDA PROTEIN IN LYSS-MECB INTERGENIC |
| | REGION | | |
| | ID2878 | S | ORF starting with ATG of length 1458 |
| | ID2879 | S | YTLR. |
| | ID2880 | S | HYPOTHETICAL 26.5 KDA PROTEIN IN RAPH-COTJA |
| | INTERGENIC REGIO | | |
| 25 | ID2881 | S | YWMB PROTEIN. |
| | ID2882 | S | YRRS PROTEIN. |
| | ID2883 | S | ORF starting with ATG of length 1443 |
| | ID2884 | S | PROTEIN BMRU. |
| 30 | ID2885 | S | ORF starting with ATG of length 1438 |
| | ID2886 | S | YDAE PROTEIN. |
| | ID2887 | S | SPORE GERMINATION PROTEIN GERD PRECURSOR. |
| | ID2888 | S | ORF starting with ATG of length 1434 |
| | ID2889 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDM. |
| 35 | ID2890 | S | SPORE GERMINATION PROTEIN A2. |
| | ID2891 | S | ORF starting with ATG of length 1431 |
| | ID2892 | S | HYPOTHETICAL 19.4 KDA PROTEIN IN SPOIIR-GLYC |
| | INTERGENIC REGI | | |
| | ID2893 | S | HYPOTHETICAL 21.9 KDA PROTEIN IN XYND-PPSE INTERGENIC |
| 40 | REGION | | |
| | ID2894 | S | HYPOTHETICAL 30.8 KDA PROTEIN IN SINI-GCVT INTERGENIC |
| | ID2895 | S | YNDL PROTEIN. |
| | ID2896 | S | HYPOTHETICAL 19.7 KDA PROTEIN. |
| 45 | ID2897 | S | HYPOTHETICAL 34.5 KDA PROTEIN IN RPLI-COTF INTERGENIC |
| | REGION | | |
| | ID2898 | S | SPORE PROTEASE (EC 3.4.99.-). |
| | ID2899 | S | Family 1 Pectate lyase.29% identical to BioPrep |
| | (SP958).50% | | |
| | ID2900 | S | STAGE II SPORULATION PROTEIN P. |
| 50 | ID2901 | S | YFLK PROTEIN. |
| | ID2902 | S | HYPOTHETICAL 16.2 KDA PROTEIN IN BMRU-ANSR INTERGENIC |
| | REGION | | |
| | ID2903 | S | GERMINATION PROTEIN GERM. |
| | ID2904 | S | ORF starting with ATG of length 1392 |
| 55 | ID2905 | S | YJBF PROTEIN. |
| | ID2906 | S | HYPOTHETICAL 19.7 KDA PROTEIN IN SPOIIR-GLYC |
| | INTERGENIC REGI | | |
| | ID2907 | S | PUTATIVE TRANSCRIPTIONAL REGULATOR (YVHJ). |
| | ID2908 | S | YYCI PROTEIN. |
| 60 | ID2909 | S | ORF starting with ATG of length 1379 |
| | ID2910 | S | YTOQ. |
| | ID2911 | S | ORF starting with ATG of length 1374 |
| | ID2912 | S | YTRI. |
| | ID2913 | S | HYPOTHETICAL 17.1 KDA PROTEIN IN SPOIIIC-CWLA |
| 65 | INTERGENIC REG | | |
| | ID2914 | S | YITE PROTEIN. |

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| | ID2915 | S | AMINOGLYCOSIDE ADENYLTRANSFERASE. |
| | ID2916 | S | COMPETENCE TRANSCRIPTION FACTOR (CTF) (COMPETENCE |
| | PROTEIN K) | | |
| 5 | ID2917 | S | HYPOTHETICAL 27.3 KDA PROTEIN IN TYRZ-SACY INTERGENIC |
| | REGION | | |
| | ID2918 | S | STAGE VI SPORULATION PROTEIN D. |
| | ID2919 | S | HYPOTHETICAL 16.6 KDA PROTEIN IN RPMF-FTSL INTERGENIC |
| | REGION | | |
| 10 | ID2920 | S | YUID PROTEIN. |
| | ID2921 | S | HYPOTHETICAL 24.8 KDA PROTEIN IN CSPB-GLPP INTERGENIC |
| | REGION | | |
| | ID2922 | S | YKUB PROTEIN. |
| | ID2923 | S | YKOK PROTEIN. |
| 15 | ID2924 | S | PEROXIDASE. |
| | ID2925 | S | SIMILAR TO BACILLUS ANTHRACIS CAPC PROTEIN. |
| | ID2926 | S | YKNT PROTEIN (CSE15 PROTEIN) (CSE15). |
| | ID2927 | S | ORF starting with ATG of length 1344 |
| | ID2928 | S | BH2938 PROTEIN. |
| 20 | ID2929 | S | HYPOTHETICAL 17.8 KDA PROTEIN IN BLTR-SPOIIIC |
| | INTERGENIC REG | | |
| | ID2930 | S | ORF starting with ATG of length 1332 |
| | ID2931 | S | TRANSCRIPTIONAL REGULATOR CTSR. |
| | ID2932 | S | HYPOTHETICAL 17.6 KDA PROTEIN IN NUSA 5'REGION (P15A) |
| | (ORF1) | | |
| 25 | ID2933 | S | ORF starting with ATG of length 1323 |
| | ID2934 | S | YOAS PROTEIN. |
| | ID2935 | S | YISF PROTEIN. |
| | ID2936 | S | STAGE II SPORULATION PROTEIN B. |
| | ID2937 | S | YTWI. |
| 30 | ID2938 | S | HYPOTHETICAL 37.0 KDA PROTEIN IN SPOIIIC-CWLA |
| | INTERGENIC REG | | |
| | ID2939 | S | YETF PROTEIN. |
| | ID2940 | S | SPAG. |
| 35 | ID2941 | S | HYPOTHETICAL 64.3 KDA PROTEIN IN HUTP-BGLP INTERGENIC |
| | REGION | | |
| | ID2942 | S | YDJH PROTEIN. |
| | ID2943 | S | YODP. |
| | ID2944 | S | YKOP. |
| 40 | ID2945 | S | HYPOTHETICAL 26.7 KDA PROTEIN IN CSBX-COXA INTERGENIC |
| | REGION | | |
| | ID2946 | S | YOCC. |
| | ID2947 | S | PUTATIVE - SOME HOMOLOGY WITH HI1034. |
| | ID2948 | S | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GSPA-TYRZ |
| 45 | ID2949 | S | HYPOTHETICAL 29.1 KDA PROTEIN. |
| | ID2950 | S | HYPOTHETICAL 23.0 KDA PROTEIN IN CMK-GPSA INTERGENIC |
| | REGION. | | |
| | ID2951 | S | SPORE PROTEASE (EC 3.4.99.-). |
| 50 | ID2952 | S | ORF starting with ATG of length 1257 |
| | ID2953 | S | CCDC PROTEIN. |
| | ID2954 | S | HYPOTHETICAL 18.4 KDA PROTEIN. |
| | ID2955 | S | HYPOTHETICAL 25.1 KDA PROTEIN IN MFD-DIVIC INTERGENIC |
| | REGION | | |
| 55 | ID2956 | S | SPORULATION INITIATION PHOSPHOTRANSFERASE B (EC 2.7.- |
| | -- (ST | | |
| | ID2957 | S | Bacillus subtilis prenyl diphosphate synthetase |
| | subunit. | | |
| | ID2958 | S | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA |
| 60 | REGION, | | |
| | ID2959 | S | HYPOTHETICAL 24.7 KDA PROTEIN IN RECQ-CMK INTERGENIC |
| | REGION. | | |
| | ID2960 | S | YMCA PROTEIN. |
| | ID2961 | S | PROBABLE PROTEIN ASP-PHOSPHATASE. |
| | ID2962 | S | ORF starting with ATG of length 1239 |
| 65 | ID2963 | S | B. subtilis hydrolase protein YQJL. |
| | ID2964 | S | ORF starting with ATG of length 1238 |

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| | ID2965 | S | ORF starting with ATG of length 1233 |
| | ID2966 | S | SIMILAR TO PHOSPHATASES. |
| | ID2967 | S | BH2308 PROTEIN. |
| 5 | ID2968 | S | HYPOTHETICAL 16.0 KDA PROTEIN IN COTF-TETB INTERGENIC REGION |
| | ID2969 | S | YKUO PROTEIN. |
| | ID2970 | S | YTLQ. |
| | ID2971 | S | YFLK PROTEIN. |
| 10 | ID2972 | S | HYPOTHETICAL 15.0 KDA PROTEIN. |
| | ID2973 | S | ORF12. |
| | ID2974 | S | YNDG PROTEIN. |
| | ID2975 | S | REQUIRED FOR REPLICATION INITIATION. |
| | ID2976 | S | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA REGION. |
| 15 | ID2977 | S | YRBG PROTEIN. |
| | ID2978 | S | YMAC PROTEIN. |
| | ID2979 | S | BH1973 PROTEIN. |
| | ID2980 | S | YNDH PROTEIN. |
| 20 | ID2981 | S | YJBB PROTEIN. |
| | ID2982 | S | GENERAL STRESS PROTEIN 26 (GSP26). |
| | ID2983 | S | ORF starting with ATG of length 1200 |
| | ID2984 | S | ORF starting with ATG of length 1200 |
| | ID2985 | S | HYPOTHETICAL 16.3 KDA PROTEIN IN TGL-PGI INTERGENIC REGION. |
| 25 | ID2986 | S | HYPOTHETICAL 19.1 KDA PROTEIN IN SPOOF-PYRG INTERGENIC REGION |
| | ID2987 | S | HYPOTHETICAL 21.1 KDA PROTEIN IN ILVA 3'REGION. |
| | ID2988 | S | HYPOTHETICAL 23.6 KDA PROTEIN IN QCRC-DAPB INTERGENIC REGION |
| 30 | ID2989 | S | STAGE III SPORULATION PROTEIN AD. |
| | ID2990 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDA. |
| | ID2991 | S | YJBK PROTEIN. |
| | ID2992 | S | CODY PROTEIN (VEGETATIVE PROTEIN 286B) (VEG286B). |
| | ID2993 | S | STAGE II SPORULATION PROTEIN M. |
| 35 | ID2994 | S | BH0621 PROTEIN. |
| | ID2995 | S | HYPOTHETICAL 17.9 KDA PROTEIN IN SPOIIIIC-CWLA INTERGENIC REG |
| | ID2996 | S | YMAC PROTEIN. |
| 40 | ID2997 | S | HYPOTHETICAL 17.0 KDA PROTEIN IN CCDC-CITB INTERGENIC REGION |
| | ID2998 | S | HYPOTHETICAL 17.5 KDA PROTEIN IN SIGV-GREA INTERGENIC REGION |
| | ID2999 | S | ORF starting with ATG of length 1155 |
| 45 | ID3000 | S | ORF starting with ATG of length 1155 |
| | ID3001 | S | YQOW PROTEIN. |
| | ID3002 | S | DNA, COMPLETE SEQUENCE. |
| | ID3003 | S | YLAJ PROTEIN. |
| | ID3004 | S | YBFI PROTEIN. |
| 50 | ID3005 | S | HYPOTHETICAL 18.1 KDA PROTEIN IN TTK-CCDA INTERGENIC REGION. |
| | ID3006 | S | ORF starting with ATG of length 1137 |
| | ID3007 | S | YESV PROTEIN. |
| | ID3008 | S | YKUD PROTEIN. |
| | ID3009 | S | STAGE III SPORULATION PROTEIN AH. |
| 55 | ID3010 | S | YKVT PROTEIN. |
| | ID3011 | S | YTFJ. |
| | ID3012 | S | ORF starting with ATG of length 1119 |
| | ID3013 | S | BH3151 PROTEIN. |
| 60 | ID3014 | S | HYPOTHETICAL 20.3 KDA PROTEIN IN UNG-ROCA INTERGENIC REGION. |
| | ID3015 | S | ORF starting with ATG of length 1116 |
| | ID3016 | S | HYPOTHETICAL 17.9 KDA PROTEIN IN DING-ASPB INTERGENIC REGION |
| | ID3017 | S | YVRI PROTEIN. |
| 65 | ID3018 | S | STAGE V SPORULATION PROTEIN AA. |
| | ID3019 | S | TRANSMEMBRANE PROTEIN. |

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| | ID3020 | S | YBBK. |
| | ID3021 | S | FTSL PROTEIN. |
| | ID3022 | S | YLOU PROTEIN. |
| | ID3023 | S | DNA REPLICATION PROTEIN DNAD. |
| 5 | ID3024 | S | YKVI PROTEIN. |
| | ID3025 | S | 4-DEOXY-L-THREO-5-HEXOSULOSE-URONATE KETOL-ISOMERASE (EC 5.3) |
| | ID3026 | S | HYPOTHETICAL 32.9 KDA PROTEIN IN CMK-GPSA INTERGENIC REGION. |
| 10 | ID3027 | S | HYPOTHETICAL 59.7 KDA PROTEIN IN CWLA-CISA INTERGENIC REGION. |
| | ID3028 | S | YUAE PROTEIN. |
| | ID3029 | S | BH0186 PROTEIN. |
| | ID3030 | S | YEEE. |
| 15 | ID3031 | S | ORF starting with ATG of length 1077 |
| | ID3032 | S | TRANSCRIPTION ANTITERMINATOR (BIGG FAMILY). |
| | ID3033 | S | HYPOTHETICAL 13.3 KDA PROTEIN IN AROD-COMER INTERGENIC REGION. |
| | ID3034 | S | BH1562 PROTEIN. |
| 20 | ID3035 | S | HYPOTHETICAL 23.9 KDA PROTEIN IN GLNQ-ANSR INTERGENIC REGION. |
| | ID3036 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDI. |
| | ID3037 | S | POSITIVE CONTROL FACTOR. |
| | ID3038 | S | HYPOTHETICAL 16.4 KDA PROTEIN. |
| 25 | ID3039 | S | BH3995 PROTEIN. |
| | ID3040 | S | YLBF PROTEIN. |
| | ID3041 | S | ORF starting with ATG of length 1065 |
| | ID3042 | S | ORF starting with ATG of length 1059 |
| | ID3043 | S | YDAT PROTEIN. |
| 30 | ID3044 | S | STAGE V SPORULATION PROTEIN AB. |
| | ID3045 | S | MLR3962 PROTEIN. |
| | ID3046 | S | YOAO. |
| | ID3047 | S | HYPOTHETICAL 14.1 KDA PROTEIN IN XPAC-ABRB INTERGENIC REGION. |
| 35 | ID3048 | S | SPORULATION-SPECIFIC EXTRACELLULAR NUCLEASE PRECURSOR (EC 3.6.1.1). |
| | ID3049 | S | YHZB PROTEIN. |
| | ID3050 | S | HYPOTHETICAL 28.8 KDA PROTEIN IN DNAJ-RPSU INTERGENIC REGION. |
| 40 | ID3051 | S | HYPOTHETICAL 23.3 KDA PROTEIN IN DNAI-THRS INTERGENIC REGION. |
| | ID3052 | S | RIBT PROTEIN. |
| | ID3053 | S | STAGE III SPORULATION PROTEIN AB. |
| | ID3054 | S | YTFL. |
| 45 | ID3055 | S | ORF starting with ATG of length 1032 |
| | ID3056 | S | METHYLASE HOMOLOG (CSPR). |
| | ID3057 | S | HYPOTHETICAL 23.3 KDA PROTEIN IN DFRA-ILVA INTERGENIC REGION. |
| | ID3058 | S | SPORE COAT PROTEIN F. |
| 50 | ID3059 | S | YAZC PROTEIN. |
| | ID3060 | S | GENERAL STRESS PROTEIN 17M (GSP17M). |
| | ID3061 | S | YKUW PROTEIN. |
| | ID3062 | S | YLBD PROTEIN. |
| | ID3063 | S | ORF starting with ATG of length 1005 |
| 55 | ID3064 | S | ORF starting with ATG of length 1002 |
| | ID3065 | S | HYPOTHETICAL 40.7 KDA PROTEIN. |
| | ID3066 | S | CHORISMATE MUTASE (EC 5.4.99.5) (CM). |
| | ID3067 | S | YUTE PROTEIN. |
| | ID3068 | S | ORF16. |
| 60 | ID3069 | S | HYPOTHETICAL 25.1 KDA PROTEIN IN PRKA 5'REGION (ORF2). |
| | ID3070 | S | HYPOTHETICAL 21.4 KDA PROTEIN IN QCRA-AROE INTERGENIC REGION. |
| | ID3071 | S | BH0817 PROTEIN. |
| 65 | ID3072 | S | CHITIN-BINDING PROTEIN. |

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| | ID3073 | S | HYPOTHETICAL 16.2 KDA PROTEIN IN COMF-FLGM INTERGENIC |
| | REGION | | |
| | ID3074 | S | ORF starting with ATG of length 984 |
| | ID3075 | S | HYPOTHETICAL 64.3 KDA PROTEIN IN HUTP-BGLP INTERGENIC |
| 5 | REGION | | |
| | ID3076 | S | HYPOTHETICAL 13.2 KDA PROTEIN IIN GUTB-COTA |
| | INTERGENIC REGION | | |
| | ID3077 | S | BH1290 PROTEIN. |
| | ID3078 | S | ORF starting with ATG of length 978 |
| 10 | ID3079 | S | HYPOTHETICAL 18.1 KDA PROTEIN IN NARK-NARG INTERGENIC |
| | REGION | | |
| | ID3080 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDJ. |
| | ID3081 | S | HYPOTHETICAL 14.0 KDA PROTEIN IN SIGV-GREA INTERGENIC |
| | REGION | | |
| 15 | ID3082 | S | YTTB. |
| | ID3083 | S | YVQK PROTEIN. |
| | ID3084 | S | YJCS PROTEIN. |
| | ID3085 | S | HYPOTHETICAL 41.5 KDA PROTEIN IN AMHX-AMYE INTERGENIC |
| | REGION | | |
| 20 | ID3086 | S | PUTATIVE PHOSPHO-BETA-GLUCOSIDASE. |
| | ID3087 | S | BH0923 PROTEIN. |
| | ID3088 | S | YVBK PROTEIN. |
| | ID3089 | S | YOAR. |
| 25 | ID3090 | S | BOFC PROTEIN PRECURSOR (BYPASS-OF-FORESPORE PROTEIN C). |
| | ID3091 | S | HYPOTHETICAL 27.7 KDA PROTEIN IN HMP-PROB INTERGENIC |
| | REGION | | |
| | ID3092 | S | HYPOTHETICAL 44.1 KDA PROTEIN. |
| | ID3093 | S | BETA-MANNOSIDASE. |
| 30 | ID3094 | S | YOEB PROTEIN. |
| | ID3095 | S | YDHG PROTEIN. |
| | ID3096 | S | HYPOTHETICAL 20.4 KDA PROTEIN IN RIBT-DACB INTERGENIC |
| | REGION | | |
| 35 | ID3097 | S | HYPOTHETICAL 48.2 KDA PROTEIN IN COTF-TETB INTERGENIC |
| | ID3098 | S | HYPOTHETICAL 30.5 KDA PROTEIN IN GABP-GUAA INTERGENIC |
| | REGION | | |
| | ID3099 | S | A AND A* PROTEINS (GPA). |
| | ID3100 | S | SIMILAR TO STAPHYLOCOCCUS AUREUS CAPA PROTEIN. |
| 40 | ID3101 | S | HYPOTHETICAL 15.7 KDA PROTEIN. |
| | ID3102 | S | YOJF PROTEIN. |
| | ID3103 | S | YVZD PROTEIN. |
| | ID3104 | S | Amino acid sequence of a spore-associated protein called Yqxs |
| 45 | ID3105 | S | YNDF PROTEIN. |
| | ID3106 | S | ORF starting with ATG of length 945 |
| | ID3107 | S | HYPOTHETICAL 39.0 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| | ID3108 | S | FENH. |
| 50 | ID3109 | S | SPORE COAT PROTEIN E. |
| | ID3110 | S | YITI PROTEIN. |
| | ID3111 | S | ORF starting with ATG of length 936 |
| | ID3112 | S | ORF starting with ATG of length 936 |
| | ID3113 | S | YLMD PROTEIN. |
| 55 | ID3114 | S | YFJM PROTEIN. |
| | ID3115 | S | BACITRACIN RESISTANCE PROTEIN (UNDECAPRENOL KINASE). |
| | ID3116 | S | YMCC PROTEIN. |
| | ID3117 | S | BH2340 PROTEIN. |
| 60 | ID3118 | S | RIBONUCLEASE PRECURSOR (EC 3.1.27.-) (BARNASE) (RNASE BA). |
| | ID3119 | S | HYPOTHETICAL 31.3 KDA PROTEIN IN LYSA-PPIB INTERGENIC |
| | REGION | | |
| | ID3120 | S | HYPOTHETICAL 19.3 KDA PROTEIN IN PONA-NTH INTERGENIC |
| | REGION | | |
| 65 | ID3121 | S | YVLD. |
| | ID3122 | S | HYPOTHETICAL 15.6 KDA PROTEIN. |

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| | ID3123 | S | BH3953 PROTEIN. |
| | ID3124 | S | HYPOTHETICAL 22.5 KDA PROTEIN IN GLYS-DNAG/DNAE |
| | INTERGENIC R | | |
| 5 | ID3125 | S | PUTATIVE SECRETED PECTINESTERASE. |
| | ID3126 | S | KINASE-ASSOCIATED PROTEIN B. |
| | ID3127 | S | YHBB PROTEIN. |
| | ID3128 | S | ORF starting with ATG of length 906 |
| | ID3129 | S | ORF starting with ATG of length 903 |
| | ID3130 | S | ORF starting with ATG of length 903 |
| 10 | ID3131 | S | HYPOTHETICAL 24.1 KDA PROTEIN IN CSPB-GLPP INTERGENIC |
| | REGION | | |
| | ID3132 | S | ORF22. |
| | ID3133 | S | HYPOTHETICAL 12.0 KDA PROTEIN IN XPAC-ABRB INTERGENIC |
| | REGION | | |
| 15 | ID3134 | S | FENI. |
| | ID3135 | S | DNA REPLICATION PROTEIN DNAD. |
| | ID3136 | S | ORF starting with ATG of length 899 |
| | ID3137 | S | YHZA HOMOLOG. |
| 20 | ID3138 | S | ORF starting with ATG of length 897 |
| | ID3139 | S | HYPOTHETICAL 25.9 KDA PROTEIN IN CCCA-SODA INTERGENIC |
| | REGION | | |
| | ID3140 | S | HYPOTHETICAL 15.6 KDA PROTEIN IN PURA-DNAC INTERGENIC |
| | REGION | | |
| 25 | ID3141 | S | HYPOTHETICAL 15.7 KDA PROTEIN IN PBPD-COMA INTERGENIC |
| | REGION | | |
| | ID3142 | S | YMDB PROTEIN. |
| | ID3143 | S | HYPOTHETICAL 13.2 KDA PROTEIN IN FTSY-FFH INTERGENIC |
| | REGION. | | |
| 30 | ID3144 | S | GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL |
| | STRESS PROTE | | |
| | ID3145 | S | YUTD PROTEIN. |
| | ID3146 | S | FLAA LOCUS 22.9 KDA PROTEIN (ORF 6). |
| | ID3147 | S | HYPOTHETICAL 10.1 KDA PROTEIN IN ORF3 5'REGION. |
| | ID3148 | S | BH3627 PROTEIN. |
| 35 | ID3149 | S | HYPOTHETICAL 18.2 KDA PROTEIN IN FLGM-FLGK INTERGENIC |
| | REGION | | |
| | ID3150 | S | YUIB PROTEIN. |
| | ID3151 | S | YCEG. |
| 40 | ID3152 | S | YDFB PROTEIN. |
| | ID3153 | S | YUSN PROTEIN. |
| | ID3154 | S | YDBL PROTEIN. |
| | ID3155 | S | YNGA PROTEIN. |
| | ID3156 | S | ORF starting with ATG of length 864 |
| | ID3157 | S | YQZD PROTEIN. |
| 45 | ID3158 | S | YERQ PROTEIN. |
| | ID3159 | S | SMALL BASIC PROTEIN. |
| | ID3160 | S | BH2308 PROTEIN. |
| | ID3161 | S | ORF starting with ATG of length 861 |
| | ID3162 | S | HYPOTHETICAL 9.5 KDA PROTEIN IN ORF3 5'REGION. |
| 50 | ID3163 | S | ORF starting with ATG of length 852 |
| | ID3164 | S | YDBS PROTEIN. |
| | ID3165 | S | ALKALINE PHOSPHATASE. |
| | ID3166 | S | HYPOTHETICAL 24.8 KDA PROTEIN IN DEGS-TAGO INTERGENIC |
| | REGION | | |
| 55 | ID3167 | S | Bacillus subtilis IFO 3336 PGA synthesising enzyme. |
| | ID3168 | S | HYPOTHETICAL 14.1 KDA PROTEIN IN PCP 5'REGION |
| | (ORF15). | | |
| | ID3169 | S | ORF starting with ATG of length 849 |
| | ID3170 | S | HYPOTHETICAL 13.1 KDA PROTEIN. |
| 60 | ID3171 | S | ORF starting with ATG of length 843 |
| | ID3172 | S | ORF starting with ATG of length 843 |
| | ID3173 | S | HYPOTHETICAL PROTEIN TC0114. |
| | ID3174 | S | HYPOTHETICAL PROTEIN VC1285. |
| | ID3175 | S | HYPOTHETICAL 16.5 KDA PROTEIN IN SPOIIR-GLYC |
| 65 | INTERGENIC REGI | | |
| | ID3176 | S | YNER. |

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| | ID3177 | S | HYPOTHETICAL 10.8 KDA PROTEIN IN RPSU-PHOH |
| | INTEREGENIC REGION | | |
| | ID3178 | S | MBL, FLH[O,P], RAPD, YWP[B,C,D,E,F,G,H,I,J] AND YWQA |
| | GENES. | | |
| 5 | ID3179 | S | COMPLETE NUCLEOTIDE SEQUENCE. |
| | ID3180 | S | HYPOTHETICAL 21.7 KDA PROTEIN IN LON-HEMA INTERGENIC |
| | REGION | | |
| | ID3181 | S | YRRD PROTEIN. |
| | ID3182 | S | YUTC PROTEIN. |
| 10 | ID3183 | S | COMPLETE NUCLEOTIDE SEQUENCE. |
| | ID3184 | S | YKRK PROTEIN. |
| | ID3185 | S | YJCA PROTEIN. |
| | ID3186 | S | HYPOTHETICAL 20.2 KDA PROTEIN IN GCVT-SPOIIIAA |
| | INTERGENIC RE | | |
| 15 | ID3187 | S | ORF starting with ATG of length 822 |
| | ID3188 | S | HYPOTHETICAL 27.7 KDA PROTEIN IN SPOIIIC-CWLA |
| | INTERGENIC REG | | |
| | ID3189 | S | ORF starting with ATG of length 822 |
| | ID3190 | S | BH3473 PROTEIN. |
| 20 | ID3191 | S | GP8 PROTEIN. |
| | ID3192 | S | YUZD PROTEIN. |
| | ID3193 | S | YRZB PROTEIN. |
| | ID3194 | S | GP8 PROTEIN. |
| | ID3195 | S | TUAF PROTEIN. |
| 25 | ID3196 | S | ORF starting with ATG of length 812 |
| | ID3197 | S | FIBRONECTIN-BINDING PROTEIN, 25KDA. |
| | ID3198 | S | YVGZ PROTEIN. |
| | ID3199 | S | PROBABLE HTH_LYSR_FAMILY TRANSCRIPTIONAL REGULATOR. |
| | ID3200 | S | YLBA PROTEIN. |
| 30 | ID3201 | S | HYPOTHETICAL 15.6 KDA PROTEIN (ORF2). |
| | ID3202 | S | ORF starting with ATG of length 800 |
| | ID3203 | S | YUEI PROTEIN. |
| | ID3204 | S | YODL. |
| | ID3205 | S | YKUK PROTEIN. |
| 35 | ID3206 | S | YLAH PROTEIN. |
| | ID3207 | S | ORF starting with ATG of length 792 |
| | ID3208 | S | YDGC PROTEIN. |
| | ID3209 | S | HYPOTHETICAL 22.3 KDA PROTEIN IN WPRA-ASNO INTERGENIC |
| | REGION | | |
| 40 | ID3210 | S | YNDE PROTEIN. |
| | ID3211 | S | ORF starting with ATG of length 783 |
| | ID3212 | S | HYPOTHETICAL 21.0 KDA LIPOPROTEIN IN CSPB-GLPP |
| | INTERGENIC RE | | |
| 45 | ID3213 | S | ORF starting with ATG of length 780 |
| | ID3214 | S | HYPOTHETICAL 19.3 KDA PROTEIN IN BCSA-DEGR INTERGENIC |
| | REGION | | |
| | ID3215 | S | HYPOTHETICAL 19.2 KDA PROTEIN. |
| | ID3216 | S | HYPOTHETICAL 64.3 KDA PROTEIN IN HUTP-BGLP INTERGENIC |
| 50 | ID3217 | S | SIMILAR TO BACILLUS SUBTILIS YXID PROTEIN. |
| | ID3218 | S | MBL, FLH[O,P], RAPD, YWP[B,C,D,E,F,G,H,I,J] AND YWQA |
| | GENES. | | |
| | ID3219 | S | YJQB PROTEIN. |
| | ID3220 | S | YDZA PROTEIN. |
| 55 | ID3221 | S | HYPOTHETICAL 13.3 KDA PROTEIN. |
| | ID3222 | S | YKUC PROTEIN. |
| | ID3223 | S | MAJOR CAPSID PROTEIN. |
| | ID3224 | S | YUBF PROTEIN. |
| | ID3225 | S | PUTATIVE PBSX REPRESSOR. |
| 60 | ID3226 | S | YTES. |
| | ID3227 | S | ORF starting with ATG of length 765 |
| | ID3228 | S | ORF starting with ATG of length 762 |
| | ID3229 | S | HYPOTHETICAL PROTEIN VC0429. |
| | ID3230 | S | CHLORAMPHENICOL ACETYLTRANSFERASE (EC 2.3.1.28) |
| 65 | (CAT). | | |

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| | ID3231 | S | HYPOTHETICAL 27.6 KDA PROTEIN IN NUCB-AROD INTERGENIC |
| | REGION | | |
| | ID3232 | S | ORF starting with ATG of length 753 |
| | ID3233 | S | YWZC PROTEIN. |
| 5 | ID3234 | S | BH0424 PROTEIN. |
| | ID3235 | S | YKOE. |
| | ID3236 | S | HYPOTHETICAL 19.8 KDA PROTEIN. |
| | ID3237 | S | YJCC PROTEIN. |
| | ID3238 | S | YFHH PROTEIN. |
| 10 | ID3239 | S | YUSQ PROTEIN. |
| | ID3240 | S | HYPOTHETICAL 9.4 KDA PROTEIN IN SODA-COMGA INTERGENIC |
| | REGION | | |
| | ID3241 | S | HYPOTHETICAL 9.9 KDA PROTEIN IN GCVT-SPOIIIAA |
| | INTERGENIC REG | | |
| 15 | ID3242 | S | YKZC PROTEIN. |
| | ID3243 | S | HYPOTHETICAL 27.7 KDA PROTEIN IN SPOIIIC-CWLA |
| | INTERGENIC REG | | |
| | ID3244 | S | BH3995 PROTEIN. |
| | ID3245 | S | BH1312 PROTEIN. |
| 20 | ID3246 | S | ORF starting with ATG of length 735 |
| | ID3247 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDH. |
| | ID3248 | S | HYPOTHETICAL 31.8 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| | ID3249 | S | YFIT PROTEIN. |
| 25 | ID3250 | S | YKUJ PROTEIN. |
| | ID3251 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDE. |
| | ID3252 | S | ORF starting with ATG of length 731 |
| | ID3253 | S | HYPOTHETICAL 10.0 KDA PROTEIN IN QOXD-VPR INTERGENIC |
| | REGION | | |
| 30 | ID3254 | S | ORF starting with ATG of length 729 |
| | ID3255 | S | YDFG PROTEIN. |
| | ID3256 | S | YDZE PROTEIN. |
| | ID3257 | S | YMFJ PROTEIN. |
| | ID3258 | S | HYPOTHETICAL 33.3 KDA PROTEIN IN KSGA-VEG INTERGENIC |
| 35 | REGION. | | |
| | ID3259 | S | ORF starting with ATG of length 720 |
| | ID3260 | S | STAGE II SPORULATION PROTEIN R. |
| | ID3261 | S | SIMILAR TO B. ANTHRACIS STERNER ELEMENT ORFA. |
| | ID3262 | S | Pectate Lyase Family 3.Putative ORF with homology to |
| 40 | this gr | | |
| | ID3263 | S | SIMILAR TO B. ANTHRACIS STERNER ELEMENT ORFA. |
| | ID3264 | S | SIMILAR TO B. ANTHRACIS STERNER ELEMENT ORFA. |
| | ID3265 | S | DNA-ENTRY NUCLEASE INHIBITOR (COMPETENCE PROTEIN J). |
| | ID3266 | S | BH1921 PROTEIN. |
| 45 | ID3267 | S | HYPOTHETICAL 14.8 KDA PROTEIN. |
| | ID3268 | S | ORF starting with ATG of length 717 |
| | ID3269 | S | YKUC PROTEIN. |
| | ID3270 | S | HYPOTHETICAL 11.0 KDA PROTEIN IN CWLL 5'REGION. |
| | ID3271 | S | HYPOTHETICAL 12.8 KDA PROTEIN IN PAIA-THR8 INTERGENIC |
| 50 | REGION | | |
| | ID3272 | S | MEMBRANE PROTEIN CSK22. |
| | ID3273 | S | ORF starting with ATG of length 714 |
| | ID3274 | S | ORF starting with ATG of length 714 |
| | ID3275 | S | HYPOTHETICAL 19.7 KDA PROTEIN IN PHEA-NIFS INTERGENIC |
| 55 | REGION | | |
| | ID3276 | S | YJCL PROTEIN. |
| | ID3277 | S | YLMC PROTEIN. |
| | ID3278 | S | ORF (FRAGMENT) . |
| | ID3279 | S | YNCE. |
| 60 | ID3280 | S | HYPOTHETICAL 9.7 KDA PROTEIN IN CWLL 5'REGION. |
| | ID3281 | S | HYPOTHETICAL 13.0 KDA PROTEIN IN IDH-DEOR INTERGENIC |
| | REGION | | |
| | ID3282 | S | YNDM PROTEIN. |
| | ID3283 | S | SIMILAR TO B. ANTHRACIS STERNER ELEMENT ORFA. |
| 65 | ID3284 | S | ORF starting with ATG of length 708 |
| | ID3285 | S | ORF starting with ATG of length 705 |

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| | ID3286 | S | HYPOTHETICAL 17.2 KDA PROTEIN. |
| | ID3287 | S | HYPOTHETICAL 21.4 KDA PROTEIN IN IDH-DEOR INTERGENIC |
| | REGION. | | |
| 5 | ID3288 | S | BH0586 PROTEIN. |
| | ID3289 | S | COMPLETE NUCLEOTIDE SEQUENCE. |
| | ID3290 | S | ORF starting with ATG of length 699 |
| | ID3291 | S | ORF starting with ATG of length 699 |
| | ID3292 | S | ORF starting with ATG of length 699 |
| | ID3293 | S | ORF starting with ATG of length 696 |
| 10 | ID3294 | S | SPORE COAT PROTEIN X. |
| | ID3295 | S | ORF starting with ATG of length 690 |
| | ID3296 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIC COMPONENT, |
| | ONE OF | | |
| 15 | ID3297 | S | HYPOTHETICAL 47.7 KDA PROTEIN IN METS-KSGA INTERGENIC |
| | REGION | | |
| | ID3298 | S | ORF starting with ATG of length 687 |
| | ID3299 | S | HYPOTHETICAL 14.6 KDA PROTEIN IN GCVT-SPOIIIAA |
| | INTERGENIC RE | | |
| 20 | ID3300 | S | HYPOTHETICAL 12.4 KDA PROTEIN IN MURC-AROA INTERGENIC |
| | REGION | | |
| | ID3301 | S | HYPOTHETICAL 49.4 KDA PROTEIN. |
| | ID3302 | S | TET.BSR. |
| | ID3303 | S | HYPOTHETICAL 17.6 KDA PROTEIN IN CWLD 5'REGION |
| | (ORF1). | | |
| 25 | ID3304 | S | YLBE PROTEIN. |
| | ID3305 | S | ORF starting with ATG of length 681 |
| | ID3306 | S | YTZH PROTEIN. |
| | ID3307 | S | SPORE COAT PROTEIN D. |
| 30 | ID3308 | S | ORF42. |
| | ID3309 | S | YDGD PROTEIN. |
| | ID3310 | S | ORF starting with ATG of length 678 |
| | ID3311 | S | ORF starting with ATG of length 675 |
| | ID3312 | S | NITRIC OXIDE SYNTHASE. |
| | ID3313 | S | STAGE III SPORULATION PROTEIN AC. |
| 35 | ID3314 | S | YETA PROTEIN. |
| | ID3315 | S | HYPOTHETICAL 21.3 KDA PROTEIN. |
| | ID3316 | S | ORF starting with ATG of length 666 |
| | ID3317 | S | BH1437 PROTEIN. |
| | ID3318 | S | YTKC. |
| 40 | ID3319 | S | HYPOTHETICAL 11.7 KDA PROTEIN IN EPR-GALK INTERGENIC |
| | REGION. | | |
| | ID3320 | S | YNDB PROTEIN. |
| | ID3321 | S | YISC PROTEIN. |
| | ID3322 | S | HYPOTHETICAL 12.7 KDA PROTEIN. |
| 45 | ID3323 | S | ORF starting with ATG of length 660 |
| | ID3324 | S | YJBL PROTEIN. |
| | ID3325 | S | HYPOTHETICAL 16.9 KDA PROTEIN. |
| | ID3326 | S | ORF starting with ATG of length 651 |
| | ID3327 | S | YISD PROTEIN. |
| 50 | ID3328 | S | ORF starting with ATG of length 652 |
| | ID3329 | S | HYPOTHETICAL 8.6 KDA PROTEIN. |
| | ID3330 | S | ORF starting with ATG of length 648 |
| | ID3331 | S | YESL PROTEIN. |
| | ID3332 | S | VEG PROTEIN. |
| 55 | ID3333 | S | ORF29. |
| | ID3334 | S | ORF starting with ATG of length 645 |
| | ID3335 | S | YUAJ PROTEIN. |
| | ID3336 | S | ORF starting with ATG of length 642 |
| | ID3337 | S | YUNC PROTEIN. |
| 60 | ID3338 | S | DNA-ENTRY NUCLEASE (EC 3.----) (COMPETENCE-SPECIFIC |
| | NUCLEAS | | |
| | ID3339 | S | ORF starting with ATG of length 639 |
| | ID3340 | S | YUZA PROTEIN. |
| | ID3341 | S | SPORE COAT PROTEIN V. |
| | ID3342 | S | YFHJ PROTEIN. |
| 65 | ID3343 | S | HYPOTHETICAL 8.5 KDA PROTEIN. |

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| | ID3344 | S | HYPOTHETICAL 9.8 KDA PROTEIN. |
| | ID3345 | S | BH2016 PROTEIN. |
| | ID3346 | S | YUSW PROTEIN. |
| | ID3347 | S | YQZG PROTEIN. |
| 5 | ID3348 | S | HYPOTHETICAL 11.8 KDA PROTEIN IN UNG-ROCA INTERGENIC REGION. |
| | ID3349 | S | YOJC. |
| | ID3350 | S | ORF starting with ATG of length 630 |
| | ID3351 | S | CSBA PROTEIN. |
| 10 | ID3352 | S | ORF starting with ATG of length 627 |
| | ID3353 | S | YLMG PROTEIN. |
| | ID3354 | S | COMPLETE NUCLEOTIDE SEQUENCE. |
| | ID3355 | S | ORF starting with ATG of length 624 |
| | ID3356 | S | ORF starting with ATG of length 624 |
| 15 | ID3357 | S | SPORE COAT PROTEIN D. |
| | ID3358 | S | ORF starting with ATG of length 621 |
| | ID3359 | S | ORF starting with ATG of length 618 |
| | ID3360 | S | YNZC PROTEIN. |
| 20 | ID3361 | S | ORF starting with ATG of length 618 |
| | ID3362 | S | YKUO PROTEIN. |
| | ID3363 | S | ORF starting with ATG of length 617 |
| | ID3364 | S | ORF starting with ATG of length 615 |
| | ID3365 | S | YCZC PROTEIN. |
| 25 | ID3366 | S | SPORE COAT PROTEIN. |
| | ID3367 | S | YRZD PROTEIN. |
| | ID3368 | S | ORF starting with ATG of length 612 |
| | ID3369 | S | HYPOTHETICAL 15.0 KDA PROTEIN IN ASNH-GNTR INTERGENIC REGION. |
| 30 | ID3370 | S | HYPOTHETICAL 9.9 KDA PROTEIN IN BCSA-DEGR INTERGENIC REGION. |
| | ID3371 | S | YRVD PROTEIN. |
| | ID3372 | S | YUEC PROTEIN. |
| | ID3373 | S | ORF starting with ATG of length 606 |
| | ID3374 | S | ORF starting with ATG of length 606 |
| 35 | ID3375 | S | HYPOTHETICAL 19.1 KDA PROTEIN IN SIGD-RPSB INTERGENIC REGION. |
| | ID3376 | S | ORF starting with ATG of length 606 |
| | ID3377 | S | HYPOTHETICAL 9.3 KDA PROTEIN IN PCKA-DPS INTERGENIC REGION. |
| 40 | ID3378 | S | ORF starting with ATG of length 603 |
| | ID3379 | S | YUEE PROTEIN. |
| | ID3380 | S | ORF starting with ATG of length 603 |
| | ID3381 | S | YOLA. |
| | ID3382 | S | YISH PROTEIN. |
| 45 | ID3383 | S | HYPOTHETICAL 30.6 KDA PROTEIN IN QCRC-DAPB INTERGENIC REGION. |
| | ID3384 | S | ORF starting with ATG of length 597 |
| | ID3385 | S | ORF starting with ATG of length 597 |
| | ID3386 | S | BH3337 PROTEIN. |
| 50 | ID3387 | S | ORF starting with ATG of length 597 |
| | ID3388 | S | BH0885 PROTEIN. |
| | ID3389 | S | HYPOTHETICAL 17.8 KDA PROTEIN. |
| | ID3390 | S | YKWD PROTEIN. |
| | ID3391 | S | ORF starting with ATG of length 591 |
| 55 | ID3392 | S | HYPOTHETICAL 25.1 KDA PROTEIN IN RECQ-CMK INTERGENIC REGION. |
| | ID3393 | S | HYPOTHETICAL 42.3 KDA PROTEIN (YVFT PROTEIN). |
| | ID3394 | S | Streptomyces galilaeus putative cyclase encoded by sgal0 gen |
| 60 | ID3395 | S | ORF starting with ATG of length 589 |
| | ID3396 | S | LYSIS PROTEIN (E PROTEIN) (GPE). |
| | ID3397 | S | HYPOTHETICAL 15.3 KDA PROTEIN IN CSPB-GLPP INTERGENIC REGION. |
| | ID3398 | S | ORF starting with ATG of length 588 |
| | ID3399 | S | YBYB PROTEIN. |
| 65 | ID3400 | S | YVLA. |

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| | ID3401 | S | YUNG PROTEIN. |
| | ID3402 | S | ORF starting with ATG of length 585 |
| | ID3403 | S | BH0588 PROTEIN. |
| | ID3404 | S | YJZC PROTEIN. |
| 5 | ID3405 | S | ORF starting with ATG of length 585 |
| | ID3406 | S | ORF starting with ATG of length 582 |
| | ID3407 | S | BH0589 PROTEIN. |
| | ID3408 | S | STAGE V SPORULATION PROTEIN AC. |
| | ID3409 | S | COMPLETE NUCLEOTIDE SEQUENCE. |
| 10 | ID3410 | S | ORF starting with ATG of length 582 |
| | ID3411 | S | ORF starting with ATG of length 579 |
| | ID3412 | S | YBFF PROTEIN. |
| | ID3413 | S | ORF starting with ATG of length 579 |
| | ID3414 | S | SMALL, ACID-SOLUBLE SPORE PROTEIN 1 (SASP). |
| 15 | ID3415 | S | HYPOTHETICAL 14.7 KDA PROTEIN IN SPOIIIC-CWLA |
| | INTERGENIC REG | | |
| | ID3416 | S | ORF starting with ATG of length 576 |
| | ID3417 | S | SIGMA-G-DEPENDENT SPORULATION SPECIFIC SASP PROTEIN. |
| | ID3418 | S | HYPOTHETICAL OXIDOREDUCTASE IN RTP-PELB INTERGENIC |
| 20 | REGION (E | | |
| | ID3419 | S | ORF starting with ATG of length 573 |
| | ID3420 | S | BH3170 PROTEIN. |
| | ID3421 | S | ORF starting with ATG of length 570 |
| | ID3422 | S | ORF starting with ATG of length 570 |
| 25 | ID3423 | S | PRODUCT REQUIRED FOR HEAD MORPHOGENESIS. |
| | ID3424 | S | ORF starting with ATG of length 567 |
| | ID3425 | S | HYPOTHETICAL 7.5 KDA PROTEIN IN CSGA 3'REGION (ORF3). |
| | ID3426 | S | YFJT PROTEIN. |
| | ID3427 | S | YUEH PROTEIN. |
| 30 | ID3428 | S | HYPOTHETICAL 14.5 KDA PROTEIN IN PONA-COTD INTERGENIC |
| | REGION | | |
| | ID3429 | S | SPORULATION CORTEX PROTEIN COXA. |
| | ID3430 | S | HYPOTHETICAL 28.3 KDA PROTEIN. |
| | ID3431 | S | HYPOTHETICAL PROTEIN. |
| 35 | ID3432 | S | HYPOTHETICAL 9.8 KDA PROTEIN IN SPOVFA 5'REGION (ORFZ). |
| | ID3433 | S | BH3870 PROTEIN. |
| | ID3434 | S | YERC PROTEIN. |
| | ID3435 | S | ORF starting with ATG of length 558 |
| 40 | ID3436 | S | HYPOTHETICAL 12.0 KDA PROTEIN IN UNG-ROCA INTERGENIC |
| | REGION. | | |
| | ID3437 | S | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YOAU. |
| | ID3438 | S | YNDF PROTEIN. |
| | ID3439 | S | HYPOTHETICAL 21.1 KDA PROTEIN IN COTD-KDUD INTERGENIC |
| 45 | REGION | | |
| | ID3440 | S | MLL7394 PROTEIN. |
| | ID3441 | S | ORF starting with ATG of length 555 |
| | ID3442 | S | CTAG PROTEIN. |
| | ID3443 | S | XPAC PROTEIN. |
| 50 | ID3444 | S | YFMB PROTEIN. |
| | ID3445 | S | YTZC PROTEIN. |
| | ID3446 | S | HYPOTHETICAL 16.7 KDA PROTEIN IN XPAC-ABRB INTERGENIC |
| | REGION | | |
| | ID3447 | S | YDJO PROTEIN. |
| 55 | ID3448 | S | HYPOTHETICAL 64.3 KDA PROTEIN IN HUTP-BGLP INTERGENIC |
| | REGION | | |
| | ID3449 | S | HYPOTHETICAL 9.2 KDA PROTEIN IN RECR-BOFA INTERGENIC |
| | REGION. | | |
| | ID3450 | S | ORF starting with TTG or GTG of length 1098 |
| 60 | ID3451 | S | ORF starting with ATG of length 549 |
| | ID3452 | S | RAPA. |
| | ID3453 | S | HYPOTHETICAL 7.3 KDA PROTEIN IN PONA-COTD INTERGENIC |
| | REGION. | | |
| | ID3454 | S | ORF starting with ATG of length 543 |
| 65 | ID3455 | S | YUSG PROTEIN. |
| | ID3456 | S | ORF starting with ATG of length 540 |

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| | ID3457 | S | BH4052 PROTEIN. |
| | ID3458 | S | ORF starting with ATG of length 537 |
| | ID3459 | S | SMALL, ACID-SOLUBLE SPORE PROTEIN A (SASP). |
| 5 | ID3460 | S | HYPOTHETICAL 10.8 KDA PROTEIN IN CCCA-SODA INTERGENIC REGION |
| | ID3461 | S | ORF starting with ATG of length 531 |
| | ID3462 | S | ORF starting with ATG of length 531 |
| | ID3463 | S | HYPOTHETICAL 11.4 KDA PROTEIN IN MFD-DIVIC INTERGENIC REGION |
| 10 | ID3464 | S | STAGE V SPORULATION PROTEIN AC. |
| | ID3465 | S | YOJB PROTEIN. |
| | ID3466 | S | HYPOTHETICAL 8.2 KDA PROTEIN IN NPRE-PYCA INTERGENIC REGION. |
| | ID3467 | S | FLAGELLAR PROTEIN REQUIRED FOR FLAGELLAR FORMATION. |
| 15 | ID3468 | S | YOED PROTEIN. |
| | ID3469 | S | ORF starting with ATG of length 525 |
| | ID3470 | S | SINI PROTEIN. |
| | ID3471 | S | YLBG PROTEIN. |
| | ID3472 | S | YEBG PROTEIN. |
| 20 | ID3473 | S | ORF starting with ATG of length 522 |
| | ID3474 | S | SORBITOL OPERON ACTIVATOR. |
| | ID3475 | S | SMALL ACID SOLUBLE SPORE PROTEIN SSPD. |
| | ID3476 | S | ORF starting with ATG of length 519 |
| | ID3477 | S | BH0695 PROTEIN. |
| 25 | ID3478 | S | CSE60. |
| | ID3479 | S | ORF starting with ATG of length 521 |
| | ID3480 | S | HYPOTHETICAL 23.2 KDA PROTEIN. |
| | ID3481 | S | YRZE PROTEIN. |
| | ID3482 | S | STAGE 0 SPORULATION PROTEIN A (SPO0A) (FRAGMENT). |
| 30 | ID3483 | S | HYPOTHETICAL 27.3 KDA PROTEIN IN RECQ-CMK INTERGENIC REGION. |
| | ID3484 | S | YFMQ. |
| | ID3485 | S | SSPF PROTEIN. |
| 35 | ID3486 | S | ORF starting with ATG of length 516 |
| | ID3487 | S | HYPOTHETICAL 15.7 KDA PROTEIN IN RPSU-PHOH INTERGENIC REGION. |
| | ID3488 | S | COMPLETE NUCLEOTIDE SEQUENCE. |
| | ID3489 | S | COMG OPERON PROTEIN 4 PRECURSOR. |
| | ID3490 | S | E22 PROTEIN (GENE 43 PROTEIN). |
| 40 | ID3491 | S | HYPOTHETICAL 10.2 KDA PROTEIN IN ILVA 3'REGION. |
| | ID3492 | S | ORF starting with ATG of length 511 |
| | ID3493 | S | HYPOTHETICAL 11.1 KDA PROTEIN YITR. |
| | ID3494 | S | ORF starting with ATG of length 513 |
| | ID3495 | S | YOZB PROTEIN. |
| 45 | ID3496 | S | HYPOTHETICAL 8.3 KDA PROTEIN IN TTK-CCDA INTERGENIC REGION. |
| | ID3497 | S | YRZG PROTEIN. |
| | ID3498 | S | HYPOTHETICAL 20.3 KDA PROTEIN. |
| | ID3499 | S | YVBJ PROTEIN. |
| 50 | ID3500 | S | BH2945 PROTEIN. |
| | ID3501 | S | HYPOTHETICAL 10.3 KDA PROTEIN. |
| | ID3502 | S | COMG OPERON PROTEIN 6. |
| | ID3503 | S | ORF starting with ATG of length 504 |
| | ID3504 | S | XPAC PROTEIN. |
| 55 | ID3505 | S | YRZA PROTEIN. |
| | ID3506 | S | ORF starting with ATG of length 504 |
| | ID3507 | S | HYPOTHETICAL 10.5 KDA PROTEIN IN ACDA 5'REGION. |
| | ID3508 | S | ORF 36 (FRAGMENT). |
| | ID3509 | S | HYPOTHETICAL 19.9 KDA PROTEIN (FRAGMENT). |
| 60 | ID3510 | S | ORF starting with ATG of length 501 |
| | ID3511 | S | YKZF PROTEIN. |
| | ID3512 | S | ORF N001. |
| | ID3513 | S | ORF starting with ATG of length 498 |
| | ID3514 | S | ORF starting with ATG of length 495 |
| 65 | ID3515 | S | HYPOTHETICAL 17.8 KDA PROTEIN. |

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| | ID3516 | S | HYPOTHETICAL 9.8 KDA PROTEIN IN HUTP-BGLP INTERGENIC |
| | REGION. | | |
| | ID3517 | S | YISG PROTEIN. |
| 5 | ID3518 | S | ORF starting with ATG of length 495 |
| | ID3519 | S | ORF starting with ATG of length 492 |
| | ID3520 | S | YKZI PROTEIN. |
| | ID3521 | S | HYPOTHETICAL 21.4 KDA PROTEIN. |
| | ID3522 | S | SIMILAR TO STAPHYLOCOCCUS AUREUS CAPA PROTEIN. |
| | ID3523 | S | BH2911 PROTEIN. |
| 10 | ID3524 | S | ORF starting with ATG of length 488 |
| | ID3525 | S | ORF starting with ATG of length 489 |
| | ID3526 | S | CSFB PROTEIN. |
| | ID3527 | S | BH2618 PROTEIN. |
| | ID3528 | S | STAGE V SPORULATION PROTEIN AE. |
| 15 | ID3529 | S | Y0ZD PROTEIN. |
| | ID3530 | S | DNA, COMPLETE SEQUENCE. |
| | ID3531 | S | YWIB PROTEIN. |
| | ID3532 | S | YOQW PROTEIN. |
| 20 | ID3533 | S | YFNK. |
| | ID3534 | S | YLAD PROTEIN. |
| | ID3535 | S | HYPOTHETICAL 6.6 KDA PROTEIN IN DING-ASPB INTERGENIC |
| | REGION. | | |
| | ID3536 | S | ORF starting with ATG of length 480 |
| 25 | ID3537 | S | HYPOTHETICAL 62.6 KDA PROTEIN IN RPMF-FTSL INTERGENIC |
| | REGION | | |
| | ID3538 | S | ORF14. |
| | ID3539 | S | BH2266 PROTEIN. |
| | ID3540 | S | ORF14. |
| 30 | ID3541 | S | ORF starting with ATG of length 478 |
| | ID3542 | S | SPORE COAT PROTEIN D. |
| | ID3543 | S | ORF starting with ATG of length 477 |
| | ID3544 | S | SIMILAR TO BACILLUS SUBTILIS YXIC PROTEIN. |
| | ID3545 | S | ORF starting with ATG of length 474 |
| | ID3546 | S | PLASMID PBS2 ORIGIN OF REPLICATION. |
| 35 | ID3547 | S | HYPOTHETICAL 20.1 KDA PROTEIN. |
| | ID3548 | S | ORF starting with ATG of length 468 |
| | ID3549 | S | ORF starting with ATG of length 468 |
| | ID3550 | S | ORF starting with ATG of length 468 |
| | ID3551 | S | GERMINATION PROTEIN. |
| 40 | ID3552 | S | OUTER MEMBRANE PORIN PROTEIN PRECURSOR. |
| | ID3553 | S | PAL-RELATED LIPOPROTEIN PRECURSOR. |
| | ID3554 | S | ORF starting with ATG of length 465 |
| | ID3555 | S | ORF starting with ATG of length 462 |
| | ID3556 | S | ORF starting with ATG of length 462 |
| 45 | ID3557 | S | ORF starting with ATG of length 462 |
| | ID3558 | S | YFKK PROTEIN. |
| | ID3559 | S | HYPOTHETICAL 38.5 KDA PROTEIN IN TNRA-SSPD INTERGENIC |
| | REGION | | |
| | ID3560 | S | SPORE COAT PROTEIN L. |
| 50 | ID3561 | S | ORF starting with ATG of length 459 |
| | ID3562 | S | DEGRADATION ENZYME REGULATION PROTEIN DEGQ (SACQ |
| | REGULATORY | | |
| | ID3563 | S | BH1955 PROTEIN. |
| | ID3564 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDD. |
| 55 | ID3565 | S | BH0893 PROTEIN. |
| | ID3566 | S | ORF starting with ATG of length 456 |
| | ID3567 | S | ORF starting with ATG of length 456 |
| | ID3568 | S | ORF starting with ATG of length 456 |
| | ID3569 | S | ORF starting with ATG of length 456 |
| 60 | ID3570 | S | ORF starting with ATG of length 456 |
| | ID3571 | S | YUZC PROTEIN. |
| | ID3572 | S | SPORE GERMINATION PROTEIN A1. |
| | ID3573 | S | ORF starting with ATG of length 453 |
| | ID3574 | S | ORF starting with ATG of length 452 |
| 65 | ID3575 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XTRA. |
| | ID3576 | S | YOLD PROTEIN. |

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| | ID3577 | S | ORF starting with ATG of length 453 |
| | ID3578 | S | ORF starting with ATG of length 453 |
| | ID3579 | S | ORF starting with ATG of length 450 |
| | ID3580 | S | ORF starting with ATG of length 981 |
| 5 | ID3581 | S | ORF starting with ATG of length 447 |
| | ID3582 | S | HYPOTHETICAL 28.0 KDA PROTEIN. |
| | ID3583 | S | ORF starting with ATG of length 447 |
| | ID3584 | S | HYPOTHETICAL 28.2 KDA PROTEIN IN CCCA-SODA INTERGENIC |
| | REGION | | |
| 10 | ID3585 | S | ORF starting with ATG of length 447 |
| | ID3586 | S | ORF starting with ATG of length 444 |
| | ID3587 | S | YKZG PROTEIN. |
| | ID3588 | S | ORF starting with ATG of length 444 |
| | ID3589 | S | ORF starting with ATG of length 444 |
| 15 | ID3590 | S | HYPOTHETICAL 8.8 KDA PROTEIN IN SPOVC-MFD INTERGENIC |
| | REGION. | | |
| | ID3591 | S | ORF starting with ATG of length 441 |
| | ID3592 | S | ORF starting with ATG of length 441 |
| | ID3593 | S | PROBABLE HTH_LYSR_FAMILY TRANSCRIPTIONAL REGULATOR. |
| 20 | ID3594 | S | ORF starting with ATG of length 438 |
| | ID3595 | S | ORF starting with ATG of length 438 |
| | ID3596 | S | PROBABLE PROTEIN ASP-PHOSPHATASE. |
| | ID3597 | S | ORF starting with ATG of length 438 |
| | ID3598 | S | ORF starting with ATG of length 438 |
| 25 | ID3599 | S | ORF starting with ATG of length 438 |
| | ID3600 | S | ORF starting with ATG of length 435 |
| | ID3601 | S | ORF starting with ATG of length 435 |
| | ID3602 | S | HYPOTHETICAL 30.6 KDA PROTEIN IN QCRC-DAPB INTERGENIC |
| | REGION | | |
| 30 | ID3603 | S | Thermotoga maritima endoglucanase. |
| | ID3604 | S | ORF starting with ATG of length 432 |
| | ID3605 | S | ORF starting with ATG of length 432 |
| | ID3606 | S | HYPOTHETICAL 9.8 KDA PROTEIN IN HUTP-BGLP INTERGENIC |
| | REGION. | | |
| 35 | ID3607 | S | SPORE COAT PROTEIN K. |
| | ID3608 | S | BH3113 PROTEIN. |
| | ID3609 | S | Sorangium cellulosum protein Orf 4. |
| | ID3610 | S | YUEG PROTEIN. |
| | ID3611 | S | HYPOTHETICAL 9.1 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| 40 | REGION. | | |
| | ID3612 | S | ORF starting with ATG of length 432 |
| | ID3613 | S | ORF starting with ATG of length 432 |
| | ID3614 | S | SIMILAR TO BACILLUS SUBTILIS YXIC PROTEIN. |
| | ID3615 | S | CAPSID PROTEIN (F PROTEIN) (GPF). |
| 45 | ID3616 | S | ORF starting with ATG of length 426 |
| | ID3617 | S | ORF starting with ATG of length 423 |
| | ID3618 | S | ORF starting with ATG of length 423 |
| | ID3619 | S | ORF starting with ATG of length 423 |
| | ID3620 | S | ORF starting with ATG of length 423 |
| 50 | ID3621 | S | ORF starting with ATG of length 423 |
| | ID3622 | S | HYPOTHETICAL 58.5 KDA PROTEIN IN SPOIIIC-CWLA |
| | INTERGENIC REG | | |
| | ID3623 | S | ORF starting with TTG or GTG of length 843 |
| | ID3624 | S | ORF starting with ATG of length 420 |
| 55 | ID3625 | S | ORF starting with ATG of length 421 |
| | ID3626 | S | ORF starting with ATG of length 420 |
| | ID3627 | S | YDAS PROTEIN. |
| | ID3628 | S | HYPOTHETICAL 15.7 KDA PROTEIN IN MURC-AROA INTERGENIC |
| | REGION | | |
| 60 | ID3629 | S | HYPOTHETICAL 25.3 KDA PROTEIN PH0221. |
| | ID3630 | S | ORF16. |
| | ID3631 | S | ORF starting with ATG of length 417 |
| | ID3632 | S | Chlamydia pneumoniae lipoprotein sequence. |
| | ID3633 | S | ORF starting with ATG of length 417 |
| 65 | ID3634 | S | COMG OPERON PROTEIN 7. |
| | ID3635 | S | ORF starting with ATG of length 414 |

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| | ID3636 | S | BH1265 PROTEIN. |
| | ID3637 | S | ORF starting with ATG of length 414 |
| | ID3638 | S | BH2053 PROTEIN. |
| 5 | ID3639 | S | ORF starting with ATG of length 411 |
| | ID3640 | S | ORF starting with ATG of length 411 |
| | ID3641 | S | HYPOTHETICAL 21.0 KDA PROTEIN IN RIBT-DACB INTERGENIC |
| | REGION | | |
| | ID3642 | S | YUEE PROTEIN. |
| 10 | ID3643 | S | HYPOTHETICAL 30.8 KDA PROTEIN IN SINI-GCVT INTERGENIC |
| | REGION | | |
| | ID3644 | S | DNA FOR 25-36 DEGREE REGION CONTAINING THE AMYE-SRFA |
| | REGION, | | |
| | ID3645 | S | ORF starting with ATG of length 409 |
| 15 | ID3646 | S | ORF starting with ATG of length 409 |
| | ID3647 | S | HYPOTHETICAL 7.6 KDA PROTEIN IN SPOIIIIC-CWLA |
| | INTERGENIC REGI | | |
| | ID3648 | S | ORF starting with ATG of length 405 |
| | ID3649 | S | ORF starting with ATG of length 405 |
| 20 | ID3650 | S | ORF starting with ATG of length 405 |
| | ID3651 | S | ORF starting with ATG of length 405 |
| | ID3652 | S | Porphyromonas gingivalis protein PG22. |
| | ID3653 | S | SMALL CORE PROTEIN (J PROTEIN). |
| | ID3654 | S | ORF starting with ATG of length 402 |
| 25 | ID3655 | S | ORF starting with ATG of length 402 |
| | ID3656 | S | ORF starting with ATG of length 399 |
| | ID3657 | S | ORF starting with ATG of length 399 |
| | ID3658 | S | ORF starting with ATG of length 399 |
| | ID3659 | S | ORF starting with ATG of length 399 |
| 30 | ID3660 | S | YFHD PROTEIN. |
| | ID3661 | S | ORF starting with ATG of length 395 |
| | ID3662 | S | HYPOTHETICAL 7.3 KDA PROTEIN IN PONA-COTD INTERGENIC |
| | REGION. | | |
| | ID3663 | S | HYPOTHETICAL 9.5 KDA PROTEIN IN ORF3 5'REGION. |
| | ID3664 | S | MRSM PROTEIN. |
| 35 | ID3665 | S | HYPOTHETICAL 16.7 KDA PROTEIN. |
| | ID3666 | S | ORF starting with ATG of length 393 |
| | ID3667 | S | ORF starting with ATG of length 393 |
| | ID3668 | S | ORF starting with ATG of length 393 |
| 40 | ID3669 | S | ORF starting with ATG of length 393 |
| | ID3670 | S | HYPOTHETICAL 31.3 KDA PROTEIN. |
| | ID3671 | S | HYPOTHETICAL PROTEIN HI1600. |
| | ID3672 | S | ORF starting with ATG of length 393 |
| | ID3673 | S | ORF starting with ATG of length 390 |
| 45 | ID3674 | S | ORF starting with ATG of length 389 |
| | ID3675 | S | ORF starting with ATG of length 387 |
| | ID3676 | S | ORF starting with ATG of length 389 |
| | ID3677 | S | ORF starting with ATG of length 387 |
| | ID3678 | S | BH2118 PROTEIN. |
| | ID3679 | S | HYPOTHETICAL 9.2 KDA PROTEIN. |
| 50 | ID3680 | S | PXO1-135. |
| | ID3681 | S | ORF starting with ATG of length 384 |
| | ID3682 | S | HYPOTHETICAL 20.5 KDA PROTEIN IN HMP-PROB INTERGENIC |
| | REGION. | | |
| | ID3683 | S | ORF starting with ATG of length 384 |
| 55 | ID3684 | S | PHI PVL ORF 63 HOMOLOGUE. |
| | ID3685 | S | SIMILAR TO B. ANTHRACIS WEYAR ELEMENT ORFB. |
| | ID3686 | S | ORF starting with ATG of length 381 |
| | ID3687 | S | ORF starting with ATG of length 381 |
| 60 | ID3688 | S | ORF starting with ATG of length 381 |
| | ID3689 | S | ORF starting with ATG of length 381 |
| | ID3690 | S | ORF starting with ATG of length 381 |
| | ID3691 | S | ORF starting with ATG of length 381 |
| | ID3692 | S | ORF starting with ATG of length 381 |
| 65 | ID3693 | S | ORF starting with ATG of length 381 |
| | ID3694 | S | ORF starting with ATG of length 381 |
| | ID3695 | S | ORF starting with ATG of length 380 |

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| | ID3696 | S | YVLB. |
| | ID3697 | S | YODN. |
| | ID3698 | S | YTEJ. |
| 5 | ID3699 | S | ORF starting with ATG of length 378 |
| | ID3700 | S | ORF starting with ATG of length 378 |
| | ID3701 | S | ORF starting with ATG of length 375 |
| | ID3702 | S | ORF starting with ATG of length 375 |
| | ID3703 | S | HYPOTHETICAL 7.5 KDA PROTEIN IN DNAC-RPLI INTERGENIC |
| | REGION. | | |
| 10 | ID3704 | S | ORF starting with ATG of length 377 |
| | ID3705 | S | ORF starting with ATG of length 375 |
| | ID3706 | S | ORF starting with ATG of length 375 |
| | ID3707 | S | YQZE PROTEIN. |
| | ID3708 | S | YFHS PROTEIN. |
| 15 | ID3709 | S | ORF starting with ATG of length 372 |
| | ID3710 | S | HYPOTHETICAL 12.8 KDA PROTEIN IN COMJ 5'REGION |
| | PRECURSOR (OR | | |
| | ID3711 | S | ORF starting with ATG of length 371 |
| | ID3712 | S | ORF starting with ATG of length 372 |
| 20 | ID3713 | S | HYPOTHETICAL 24.6 KDA PROTEIN IN DAE-TYRZ INTERGENIC |
| | REGION. | | |
| | ID3714 | S | HYPOTHETICAL 9.8 KDA PROTEIN. |
| | ID3715 | S | ORF starting with ATG of length 369 |
| | ID3716 | S | ORF starting with ATG of length 369 |
| 25 | ID3717 | S | YJCF PROTEIN. |
| | ID3718 | S | BH0973 PROTEIN. |
| | ID3719 | S | HYPOTHETICAL 14.9 KDA PROTEIN. |
| | ID3720 | S | ORF starting with ATG of length 368 |
| | ID3721 | S | ORF starting with ATG of length 369 |
| 30 | ID3722 | S | ORF starting with ATG of length 366 |
| | ID3723 | S | ORF starting with ATG of length 366 |
| | ID3724 | S | ORF starting with ATG of length 366 |
| | ID3725 | S | ORF starting with ATG of length 366 |
| | ID3726 | S | ORF starting with ATG of length 363 |
| 35 | ID3727 | S | ORF starting with ATG of length 363 |
| | ID3728 | S | ORF starting with ATG of length 363 |
| | ID3729 | S | ORF starting with ATG of length 363 |
| | ID3730 | S | ORF starting with ATG of length 365 |
| | ID3731 | S | ORF starting with ATG of length 364 |
| 40 | ID3732 | S | (CLONE LAMBDA-BS1) CELL DIVISION AND SPORULATION |
| | PROTEIN (DD | | |
| | ID3733 | S | ORF starting with ATG of length 363 |
| | ID3734 | S | ORF starting with ATG of length 363 |
| | ID3735 | S | ORF starting with ATG of length 363 |
| 45 | ID3736 | S | ORF starting with ATG of length 363 |
| | ID3737 | S | HYPOTHETICAL 7.1 KDA PROTEIN IN RECQ-CMK INTERGENIC |
| | REGION. | | |
| | ID3738 | S | NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4) |
| | (GLUTAMAT | | |
| 50 | ID3739 | S | POSITIVE TRANSCRIPTIONAL ACTIVATOR. |
| | ID3740 | S | YOLD PROTEIN. |
| | ID3741 | S | ORF starting with ATG of length 360 |
| | ID3742 | S | ORF starting with ATG of length 360 |
| | ID3743 | S | DIVISION INITIATION PROTEIN (DIVIB) (FRAGMENT). |
| 55 | ID3744 | S | POTENTIAL ABC TRANSPORTER. |
| | ID3745 | S | ORF starting with TTG or GTG of length 711 |
| | ID3746 | S | ORF starting with ATG of length 357 |
| | ID3747 | S | ORF starting with ATG of length 357 |
| | ID3748 | S | ORF starting with ATG of length 357 |
| 60 | ID3749 | S | GENOMIC DNA, CHROMOSOME 3, BAC CLONE:F1D9. |
| | ID3750 | S | ORF starting with ATG of length 357 |
| | ID3751 | S | ORF starting with ATG of length 357 |
| | ID3752 | S | ORF starting with TTG or GTG of length 708 |
| | ID3753 | S | ORF starting with ATG of length 354 |
| 65 | ID3754 | S | VCO28. |
| | ID3755 | S | ORF starting with ATG of length 354 |

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| | ID3756 | S | ORF starting with ATG of length 351 |
| | ID3757 | S | ORF starting with ATG of length 353 |
| | ID3758 | S | ORF starting with ATG of length 351 |
| | ID3759 | S | ORF starting with ATG of length 351 |
| 5 | ID3760 | S | ORF starting with ATG of length 351 |
| | ID3761 | S | <i>Bacillus licheniformis</i> (BLC) RP-II protease. |
| | ID3762 | S | HYPOTHETICAL 29.5 KDA PROTEIN IN ROCC-PTA INTERGENIC |
| | REGION. | | |
| 10 | ID3763 | S | ORF starting with ATG of length 348 |
| | ID3764 | S | YOMP PROTEIN. |
| | ID3765 | S | PROBABLE HTH_ARAC_FAMILY OF TRANSCRIPTIONAL |
| | REGULATOR. | | |
| | ID3766 | S | SPORE COAT PROTEIN. |
| 15 | ID3767 | S | ORF starting with ATG of length 345 |
| | ID3768 | S | ORF starting with ATG of length 345 |
| | ID3769 | S | HYPOTHETICAL 6.9 KDA PROTEIN IN SODA-COMGA INTERGENIC |
| | REGION | | |
| | ID3770 | S | ORF starting with ATG of length 345 |
| | ID3771 | S | PUTATIVE PERMEASE. |
| 20 | ID3772 | S | YKZB PROTEIN. |
| | ID3773 | S | ORF starting with ATG of length 345 |
| | ID3774 | S | YKZE PROTEIN. |
| | ID3775 | S | ORF starting with ATG of length 342 |
| 25 | ID3776 | S | ORF starting with ATG of length 342 |
| | ID3777 | S | ORF starting with ATG of length 342 |
| | ID3778 | S | ORF starting with ATG of length 339 |
| | ID3779 | S | ORF starting with ATG of length 339 |
| | ID3780 | S | ORF starting with ATG of length 339 |
| | ID3781 | S | ORF starting with ATG of length 339 |
| 30 | ID3782 | S | BH0644 PROTEIN. |
| | ID3783 | S | ORF starting with ATG of length 339 |
| | ID3784 | S | ORF starting with ATG of length 339 |
| | ID3785 | S | YDCC PROTEIN. |
| | ID3786 | S | ORF starting with ATG of length 339 |
| 35 | ID3787 | S | ORF starting with ATG of length 339 |
| | ID3788 | S | ORF starting with ATG of length 339 |
| | ID3789 | S | ORF starting with ATG of length 339 |
| | ID3790 | S | ORF starting with ATG of length 339 |
| | ID3791 | S | ORF starting with ATG of length 341 |
| 40 | ID3792 | S | YFLB PROTEIN. |
| | ID3793 | S | ORF starting with ATG of length 335 |
| | ID3794 | S | BH0315 PROTEIN. |
| | ID3795 | S | ORF starting with ATG of length 336 |
| | ID3796 | S | YOAF PROTEIN. |
| 45 | ID3797 | S | SIMILAR TO <i>B. ANTHRACIS</i> WEYAR ELEMENT ORFB. |
| | ID3798 | S | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YYBE. |
| | ID3799 | S | ORF starting with ATG of length 333 |
| | ID3800 | S | ORF starting with ATG of length 333 |
| | ID3801 | S | HYPOTHETICAL 7.5 KDA PROTEIN IN GPSA-SPOIVA |
| 50 | INTERGENIC REGION | | |
| | ID3802 | S | ORF starting with ATG of length 333 |
| | ID3803 | S | HYPOTHETICAL 21.0 KDA PROTEIN IN RIBT-DACB INTERGENIC |
| | REGION | | |
| | ID3804 | S | ORF starting with ATG of length 333 |
| 55 | ID3805 | S | ORF starting with ATG of length 333 |
| | ID3806 | S | ORF starting with ATG of length 333 |
| | ID3807 | S | ORF starting with ATG of length 333 |
| | ID3808 | S | HYPOTHETICAL 18.8 KDA PROTEIN PH0220. |
| | ID3809 | S | ORF starting with ATG of length 330 |
| 60 | ID3810 | S | ORF starting with TTG or GTG of length 660 |
| | ID3811 | S | REPRESSOR. |
| | ID3812 | S | ORF starting with ATG of length 327 |
| | ID3813 | S | ORF starting with ATG of length 327 |
| | ID3814 | S | ORF starting with TTG or GTG of length 651 |
| 65 | ID3815 | S | HYPOTHETICAL 4.5 KDA PROTEIN. |
| | ID3816 | S | ORF starting with ATG of length 324 |

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| | ID3817 | S | YNZD PROTEIN. |
| | ID3818 | S | EATRO 164 KINETOPLAST (CR4). |
| | ID3819 | S | HYPOTHETICAL 18.8 KDA PROTEIN PH0220. |
| | ID3820 | S | GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC |
| 5 | 1.2.1.41) (GLUT | | |
| | ID3821 | S | ORF starting with ATG of length 324 |
| | ID3822 | S | ORF starting with ATG of length 324 |
| | ID3823 | S | ORF starting with ATG of length 1059 |
| | ID3824 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDW. |
| 10 | ID3825 | S | 403AA LONG HYPOTHETICAL COENZYME PQQ SYNTHESIS |
| | PROTEIN. | | |
| | ID3826 | S | ORF starting with ATG of length 321 |
| | ID3827 | S | ORF starting with ATG of length 319 |
| | ID3828 | S | ORF starting with ATG of length 321 |
| 15 | ID3829 | S | ORF starting with ATG of length 321 |
| | ID3830 | S | YKZH PROTEIN. |
| | ID3831 | S | ORF starting with ATG of length 318 |
| | ID3832 | S | ORF starting with ATG of length 318 |
| | ID3833 | S | BH1226 PROTEIN. |
| 20 | ID3834 | S | ORF starting with ATG of length 318 |
| | ID3835 | S | FLAGELLAR PROTEIN FLIT. |
| | ID3836 | S | YFLJ PROTEIN. |
| | ID3837 | S | ORF starting with ATG of length 318 |
| | ID3838 | S | ORF starting with TTG or GTG of length 633 |
| 25 | ID3839 | S | ORF starting with ATG of length 315 |
| | ID3840 | S | ORF starting with ATG of length 315 |
| | ID3841 | S | ORF starting with ATG of length 315 |
| | ID3842 | S | HYPOTHETICAL 6.3 KDA PROTEIN IN SODA-COMGA INTERGENIC |
| | REGION | | |
| 30 | ID3843 | S | ORF21. |
| | ID3844 | S | LACA. |
| | ID3845 | S | ORF starting with ATG of length 315 |
| | ID3846 | S | ORF starting with ATG of length 315 |
| | ID3847 | S | CYTOCHROME AA3 CONTROLLING PROTEIN. |
| 35 | ID3848 | S | YVKN. |
| | ID3849 | S | ORF starting with ATG of length 312 |
| | ID3850 | S | ORF starting with ATG of length 313 |
| | ID3851 | S | ORF starting with ATG of length 312 |
| | ID3852 | S | HYPOTHETICAL 19.5 KDA PROTEIN IN DEGA-NPRB INTERGENIC |
| 40 | REGION | | |
| | ID3853 | S | ORF starting with ATG of length 311 |
| | ID3854 | S | ORF starting with ATG of length 312 |
| | ID3855 | S | QUINOLONE RESISTANCE PROTEIN. |
| | ID3856 | S | YEEF PROTEIN. |
| 45 | ID3857 | S | HYPOTHETICAL 18.8 KDA PROTEIN PH0220. |
| | ID3858 | S | ORF starting with ATG of length 313 |
| | ID3859 | S | ORF starting with ATG of length 312 |
| | ID3860 | S | ORF starting with ATG of length 312 |
| | ID3861 | S | ORF starting with TTG or GTG of length 621 |
| 50 | ID3862 | S | ORF starting with ATG of length 309 |
| | ID3863 | S | YUIA PROTEIN. |
| | ID3864 | S | YRZK PROTEIN. |
| | ID3865 | S | IOLB PROTEIN. |
| | ID3866 | S | BH1709 PROTEIN. |
| 55 | ID3867 | S | BH0952 PROTEIN. |
| | ID3868 | S | PHOSPHATIDYL SERINE SYNTHASE. |
| | ID3869 | S | HYPOTHETICAL 17.9 KDA PROTEIN IN RECQ-CMK INTERGENIC |
| | REGION. | | |
| | ID3870 | S | ORF starting with ATG of length 306 |
| 60 | ID3871 | S | REPRESSOR |
| | ID3872 | S | ORF starting with ATG of length 353 |
| | ID3873 | S | ORF starting with ATG of length 306 |
| | ID3874 | S | ORF starting with ATG of length 306 |
| | ID3875 | S | ORF starting with ATG of length 303 |
| 65 | ID3876 | S | ORF starting with ATG of length 303 |
| | ID3877 | S | ORF starting with ATG of length 303 |

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| | ID3878 | S | ORF starting with ATG of length 303 |
| | ID3879 | S | CYTOCHROME C-550. |
| | ID3880 | S | YOSA PROTEIN. |
| 5 | ID3881 | S | Thymidylate kinase-2. |
| | ID3882 | S | HYPOTHETICAL 13.7 KDA PROTEIN. |
| | ID3883 | S | ORF starting with ATG of length 300 |
| | ID3884 | S | ORF starting with ATG of length 301 |
| | ID3885 | S | ORF starting with ATG of length 300 |
| 10 | ID3886 | S | ORF starting with ATG of length 300 |
| | ID3887 | S | YUNB PROTEIN. |
| | ID3888 | S | BH3172 PROTEIN. |
| | ID3889 | S | ORF starting with ATG of length 300 |
| | ID3890 | S | ORF starting with ATG of length 300 |
| 15 | ID3891 | S | HYPOTHETICAL 10.9 KDA PROTEIN. |
| | ID3892 | S | ORF starting with ATG of length 333 |
| | ID3893 | S | ORF starting with ATG of length 298 |
| | ID3894 | S | YOMM PROTEIN. |
| | ID3895 | S | ORF starting with ATG of length 297 |
| 20 | ID3896 | S | PLASMID PAM-BETA1 ADENINE METHYLASE GENE (FRAGMENT). |
| | ID3897 | S | HYPOTHETICAL 42.0 KDA PROTEIN IN DAPB-PAPS INTERGENIC REGION |
| | ID3898 | S | YVQI PROTEIN. |
| | ID3899 | S | ORF starting with ATG of length 297 |
| | ID3900 | S | ORF starting with ATG of length 297 |
| 25 | ID3901 | S | GLYCINE-RICH PROTEIN PRECURSOR. |
| | ID3902 | S | ORF starting with ATG of length 294 |
| | ID3903 | S | ORF starting with ATG of length 294 |
| | ID3904 | S | YOZM PROTEIN. |
| 30 | ID3905 | S | ORF starting with ATG of length 294 |
| | ID3906 | S | ORF starting with ATG of length 291 |
| | ID3907 | S | ORF starting with ATG of length 291 |
| | ID3908 | S | ORF starting with ATG of length 291 |
| | ID3909 | S | HYPOTHETICAL 23.2 KDA PROTEIN. |
| 35 | ID3910 | S | HYPOTHETICAL 16.5 KDA PROTEIN. |
| | ID3911 | S | ORF starting with ATG of length 291 |
| | ID3912 | S | ORF starting with ATG of length 288 |
| | ID3913 | S | ORF starting with ATG of length 288 |
| | ID3914 | S | ORF starting with ATG of length 288 |
| 40 | ID3915 | S | ORF starting with ATG of length 288 |
| | ID3916 | S | CDP-DIACYLGlycerol--SERINE O-PHOSPHATIDYLTRANSFERASE (EC 2.7) |
| | ID3917 | S | ORF starting with ATG of length 288 |
| | ID3918 | S | HPR(SER) KINASE/PHOSPHATASE (EC 2.7.1.-) (EC 3.1.3.-) |
| 45 |) | | |
| | ID3919 | S | MLR7758 PROTEIN. |
| | ID3920 | S | L-ASPARTATE OXIDASE (EC 1.4.3.16) (QUINOLINATE SYNTHETASE B) |
| | ID3921 | S | HYPOTHETICAL 23.3 KDA PROTEIN IN ROCC-PTA INTERGENIC REGION. |
| 50 | ID3922 | S | BH0606 PROTEIN. |
| | ID3923 | S | ORF starting with ATG of length 285 |
| | ID3924 | S | ORF starting with TTG or GTG of length 569 |
| | ID3925 | S | LANTIBIOTIC MERSACIDIN PRECURSOR. |
| 55 | ID3926 | S | ORF starting with ATG of length 285 |
| | ID3927 | S | ORF starting with ATG of length 285 |
| | ID3928 | S | ORF starting with ATG of length 285 |
| | ID3929 | S | ORF starting with ATG of length 285 |
| | ID3930 | S | ORF starting with ATG of length 285 |
| 60 | ID3931 | S | ORF starting with ATG of length 282 |
| | ID3932 | S | ORF starting with ATG of length 282 |
| | ID3933 | S | ORF starting with ATG of length 282 |
| | ID3934 | S | ORF starting with ATG of length 282 |
| | ID3935 | S | PROLINE PERMEASE. |
| | ID3936 | S | ORF starting with ATG of length 282 |
| 65 | ID3937 | S | STRESS RESPONSE HOMOLOG HSP. |
| | ID3938 | S | ORF starting with ATG of length 279 |

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| | ID3939 | S | ORF starting with ATG of length 279 |
| | ID3940 | S | ORF starting with ATG of length 279 |
| | ID3941 | S | HYPOTHETICAL 4.0 KDA PROTEIN. |
| 5 | ID3942 | S | ORF starting with ATG of length 279 |
| | ID3943 | S | YUBI PROTEIN. |
| | ID3944 | S | ORF starting with ATG of length 276 |
| | ID3945 | S | ORF42. |
| | ID3946 | S | ORF starting with ATG of length 276 |
| | ID3947 | S | TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA |
| 10 | PSEUDOURID | | |
| | ID3948 | S | HYPOTHETICAL 73.6 KDA PROTEIN. |
| | ID3949 | S | Human protein sequence SEQ ID NO:11751. |
| | ID3950 | S | ORF starting with ATG of length 273 |
| 15 | ID3951 | S | HYPOTHETICAL 22.4 KDA PROTEIN IN RPMF-FTSL INTERGENIC REGION |
| | ID3952 | S | BH2341 PROTEIN. |
| | ID3953 | S | Right origin-binding protein. |
| | ID3954 | S | ORF starting with ATG of length 273 |
| 20 | ID3955 | S | ORF starting with ATG of length 273 |
| | ID3956 | S | ORF starting with ATG of length 273 |
| | ID3957 | S | ORF starting with ATG of length 270 |
| | ID3958 | S | ORF starting with ATG of length 270 |
| | ID3959 | S | ORF starting with ATG of length 270 |
| | ID3960 | S | YDBN PROTEIN. |
| 25 | ID3961 | S | DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN (DRRA-1). |
| | ID3962 | S | ORF starting with ATG of length 270 |
| | ID3963 | S | ORF starting with ATG of length 267 |
| | ID3964 | S | ORF starting with ATG of length 267 |
| 30 | ID3965 | S | ORF starting with ATG of length 267 |
| | ID3966 | S | ORF starting with ATG of length 267 |
| | ID3967 | S | BH2327 PROTEIN. |
| | ID3968 | S | HYPOTHETICAL 30.7 KDA LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION |
| 35 | ID3969 | S | HYPOTHETICAL 17.1 KDA PROTEIN IN RAPH-COTJA INTERGENIC REGION |
| | ID3970 | S | YLBB PROTEIN. |
| | ID3971 | S | ORF starting with TTG or GTG of length 530 |
| | ID3972 | S | METHYLTRANSFERASE/UROPORPHYRINOGEN-III SYNTHASE. |
| | ID3973 | S | HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION. |
| 40 | ID3974 | S | ORF starting with ATG of length 264 |
| | ID3975 | S | ORF starting with ATG of length 264 |
| | ID3976 | S | ORF starting with ATG of length 264 |
| | ID3977 | S | ORF starting with ATG of length 264 |
| 45 | ID3978 | S | YOBG. |
| | ID3979 | S | ORF starting with ATG of length 261 |
| | ID3980 | S | ORF starting with ATG of length 261 |
| | ID3981 | S | ORF starting with ATG of length 261 |
| | ID3982 | S | ORF starting with ATG of length 261 |
| 50 | ID3983 | S | ORF starting with ATG of length 261 |
| | ID3984 | S | ORF starting with TTG or GTG of length 522 |
| | ID3985 | S | ORF starting with ATG of length 259 |
| | ID3986 | S | BH1397 PROTEIN. |
| | ID3987 | S | YFIQ PROTEIN. |
| 55 | ID3988 | S | ORF starting with ATG of length 259 |
| | ID3989 | S | YYZB PROTEIN. |
| | ID3990 | S | HYPOTHETICAL 6.0 KDA PROTEIN. |
| | ID3991 | S | ORF starting with ATG of length 261 |
| | ID3992 | S | 50S RIBOSOMAL PROTEIN L2 (BL2). |
| 60 | ID3993 | S | YQZH PROTEIN. |
| | ID3994 | S | ORF starting with ATG of length 258 |
| | ID3995 | S | HYPOTHETICAL 12.8 KDA PROTEIN. |
| | ID3996 | S | IMMUNOGENIC PROTEIN. |
| 65 | ID3997 | S | ORF starting with ATG of length 258 |
| | ID3998 | S | BH1336 PROTEIN. |
| | ID3999 | S | BH2912 PROTEIN. |

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| | ID4000 | S | ORF starting with ATG of length 258 |
| | ID4001 | S | ORF starting with ATG of length 258 |
| | ID4002 | S | HYPOTHETICAL 8.7 KDA PROTEIN. |
| | ID4003 | S | YDBT PROTEIN. |
| 5 | ID4004 | S | ORF starting with ATG of length 255 |
| | ID4005 | S | ORF starting with ATG of length 255 |
| | ID4006 | S | BH0426 PROTEIN. |
| | ID4007 | S | BH0636 PROTEIN. |
| | ID4008 | S | HYPOTHETICAL 6.3 KDA PROTEIN. |
| 10 | ID4009 | S | ORF starting with ATG of length 255 |
| | ID4010 | S | ORF starting with ATG of length 255 |
| | ID4011 | S | YFL1 PROTEIN. |
| | ID4012 | S | EBV tethering protein EBNA1. |
| | ID4013 | S | BH1502 PROTEIN. |
| 15 | ID4014 | S | HYPOTHETICAL 8.5 KDA PROTEIN (FRAGMENT). |
| | ID4015 | S | OCTAPEPTIDE-REPEAT PROTEIN T2. |
| | ID4016 | S | ORF starting with ATG of length 252 |
| | ID4017 | S | SIGNAL PEPTIDASE I P (EC 3.4.21.89) (SPASE I) (LEADER |
| | PEPTID | | |
| 20 | ID4018 | S | ORF starting with ATG of length 252 |
| | ID4019 | S | ORF starting with ATG of length 252 |
| | ID4020 | S | PUTATIVE - SOME HOMOLOGY WITH METH2. |
| | ID4021 | S | SITE-SPECIFIC RECOMBINASE XERC. |
| | ID4022 | S | Arabidopsis thaliana protein fragment SEQ ID NO: |
| | 48115. | | |
| | ID4023 | S | ORF starting with ATG of length 252 |
| | ID4024 | S | ORF starting with ATG of length 252 |
| | ID4025 | S | ORF starting with ATG of length 252 |
| | ID4026 | S | HYPOTHETICAL 42.6 KDA PROTEIN IN BSAA-ILVD INTERGENIC |
| 30 | REGION | | |
| | ID4027 | S | SA1216 PROTEIN. |
| | ID4028 | S | REGULATORY PROTEIN GLNR. |
| | ID4029 | S | ORF starting with ATG of length 249 |
| | ID4030 | S | ORF starting with ATG of length 248 |
| 35 | ID4031 | S | ORF starting with ATG of length 249 |
| | ID4032 | S | ORF starting with ATG of length 249 |
| | ID4033 | S | ORF starting with ATG of length 249 |
| | ID4034 | S | ORF starting with ATG of length 249 |
| | ID4035 | S | 30S RIBOSOMAL PROTEIN S21. |
| 40 | ID4036 | S | YFMJ PROTEIN. |
| | ID4037 | S | STAGE V SPORULATION PROTEIN M. |
| | ID4038 | S | ORF starting with ATG of length 249 |
| | ID4039 | S | ORF starting with ATG of length 249 |
| | ID4040 | S | ORF starting with ATG of length 249 |
| 45 | ID4041 | S | ORF starting with ATG of length 249 |
| | ID4042 | S | ORF starting with ATG of length 249 |
| | ID4043 | S | ORF starting with ATG of length 246 |
| | ID4044 | S | VMP3 PROTEIN. |
| | ID4045 | S | ORF starting with ATG of length 246 |
| 50 | ID4046 | S | ORF starting with ATG of length 246 |
| | ID4047 | S | ORF starting with ATG of length 246 |
| | ID4048 | S | ORF starting with ATG of length 246 |
| | ID4049 | S | ORF starting with ATG of length 243 |
| | ID4050 | S | PUTATIVE TRANSPOSSASE. |
| 55 | ID4051 | S | Human protein sequence SEQ ID NO:17122. |
| | ID4052 | S | ORF starting with ATG of length 243 |
| | ID4053 | S | ORF starting with ATG of length 243 |
| | ID4054 | S | HYDROXYPROLINE-RICH PROTEIN. |
| | ID4055 | S | HYPOTHETICAL 34.8 KDA PROTEIN. |
| 60 | ID4056 | S | T08D2.8 PROTEIN. |
| | ID4057 | S | PBSX PHAGE TERMINASE LARGE SUBUNIT. |
| | ID4058 | S | ORF starting with ATG of length 240 |
| | ID4059 | S | ORF starting with ATG of length 240 |
| | ID4060 | S | ORF starting with ATG of length 240 |
| 65 | ID4061 | S | HYPOTHETICAL 40.9 KDA PROTEIN IN MECB-GLTX INTERGENIC |
| | REGION | | |

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| | ID4062 | S | YWIB PROTEIN. |
| | ID4063 | S | PROLINE-RICH PROTEIN. |
| | ID4064 | S | CG2839 PROTEIN (FRAGMENT). |
| | ID4065 | S | NADH DEHYDROGENASE (EC 1.6.99.3) (ALKYL HYDROPEROXIDE |
| 5 | REDUCT | | |
| | ID4066 | S | HSDS. |
| | ID4067 | S | SP62_HUMAN. |
| | ID4068 | S | HYPOTHETICAL 7.7 KDA PROTEIN IN ILVA 3'REGION. |
| | ID4069 | S | ORF starting with ATG of length 237 |
| 10 | ID4070 | S | YCZF PROTEIN. |
| | ID4071 | S | ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE--TRNA |
| | LIGASE) | (| |
| | ID4072 | S | TRANSPOSON TN10 TETD PROTEIN (ORFR). |
| | ID4073 | S | ORF starting with ATG of length 237 |
| 15 | ID4074 | S | ORF starting with ATG of length 234 |
| | ID4075 | S | ORF starting with ATG of length 234 |
| | ID4076 | S | ORF starting with ATG of length 234 |
| | ID4077 | S | HYPOTHETICAL 18.5 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC | REGIO | |
| 20 | ID4078 | S | ORF starting with ATG of length 234 |
| | ID4079 | S | DNA BINDING PROTEIN. |
| | ID4080 | S | ORF starting with ATG of length 234 |
| | ID4081 | S | ORF starting with ATG of length 234 |
| | ID4082 | S | ORF starting with ATG of length 234 |
| 25 | ID4083 | S | ORF starting with ATG of length 234 |
| | ID4084 | S | ORF starting with ATG of length 234 |
| | ID4085 | S | ORF starting with ATG of length 234 |
| | ID4086 | S | ORF starting with ATG of length 234 |
| | ID4087 | S | ORF starting with ATG of length 231 |
| 30 | ID4088 | S | ORF starting with ATG of length 231 |
| | ID4089 | S | ORF starting with ATG of length 231 |
| | ID4090 | S | TRNA LIGASE (EC 6.5.1.3). |
| | ID4091 | S | ORF starting with ATG of length 375 |
| | ID4092 | S | HYPOTHETICAL 48.6 KDA PROTEIN IN SERS-DNAZ INTERGENIC |
| 35 | REGION | | |
| | ID4093 | S | ORF starting with ATG of length 231 |
| | ID4094 | S | ORF starting with ATG of length 231 |
| | ID4095 | S | ORF starting with ATG of length 231 |
| | ID4096 | S | ORF starting with ATG of length 231 |
| 40 | ID4097 | S | CELL DEATH REGULATOR AVEN. |
| | ID4098 | S | ORF starting with TTG or GTG of length 460 |
| | ID4099 | S | BH0850 PROTEIN. |
| | ID4100 | S | HYPOTHETICAL 21.0 KDA PROTEIN IN TLP-GRLB INTERGENIC |
| | REGION. | | |
| 45 | ID4101 | S | BH1321 PROTEIN. |
| | ID4102 | S | ORF starting with ATG of length 228 |
| | ID4103 | S | ORF starting with ATG of length 228 |
| | ID4104 | S | ORF starting with ATG of length 228 |
| | ID4105 | S | KIAA1297 PROTEIN (FRAGMENT). |
| 50 | ID4106 | S | HYPOTHETICAL 15.9 KDA PROTEIN. |
| | ID4107 | S | HYPOTHETICAL 24.5 KDA PROTEIN. |
| | ID4108 | S | ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9). |
| | ID4109 | S | ORF starting with ATG of length 228 |
| | ID4110 | S | ORF starting with ATG of length 228 |
| 55 | ID4111 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC ENZYME IIA |
| | COMPONENT. | | |
| | ID4112 | S | ORF33. |
| | ID4113 | S | YNZH PROTEIN. |
| | ID4114 | S | ODHA (EC 1.2.4.2) (OXOGLUTARATE DEHYDROGENASE |
| 60 | (LIPOAMIDE)) | (O | |
| | ID4115 | S | YOST PROTEIN. |
| | ID4116 | S | ORF starting with ATG of length 225 |
| | ID4117 | S | ORF starting with ATG of length 225 |
| | ID4118 | S | ORF starting with ATG of length 225 |
| | ID4119 | S | ORF starting with ATG of length 225 |
| 65 | ID4120 | S | ORF starting with ATG of length 225 |

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| | ID4121 | S | ORF starting with ATG of length 225 |
| | ID4122 | S | BH1397 PROTEIN. |
| | ID4123 | S | P-HYDROXYBENZOATE HYDROXYLASE (EC 1.14.13.2) (4- |
| | HYDROXYBENZO | | |
| 5 | ID4124 | S | ORF starting with ATG of length 225 |
| | ID4125 | S | ORF starting with ATG of length 225 |
| | ID4126 | S | ORF starting with TTG or GTG of length 447 |
| | ID4127 | S | ORF starting with ATG of length 225 |
| | ID4128 | S | ORF starting with ATG of length 225 |
| 10 | ID4129 | S | ORF starting with ATG of length 222 |
| | ID4130 | S | ORF starting with ATG of length 222 |
| | ID4131 | S | YFKG. |
| | ID4132 | S | ORF starting with ATG of length 222 |
| | ID4133 | S | ORF starting with ATG of length 222 |
| 15 | ID4134 | S | UNIDENTIFIED TRANSPORTER-ATP BINDING. |
| | ID4135 | S | HYPOTHETICAL 11.5 KDA PROTEIN PH0217. |
| | ID4136 | S | HYPOTHETICAL 7.3 KDA PROTEIN. |
| | ID4137 | S | ORF starting with ATG of length 222 |
| | ID4138 | S | YUTJ PROTEIN. |
| 20 | ID4139 | S | ORF starting with ATG of length 222 |
| | ID4140 | S | ORF starting with ATG of length 222 |
| | ID4141 | S | ORF starting with ATG of length 219 |
| | ID4142 | S | ORF starting with ATG of length 219 |
| | ID4143 | S | ORF starting with ATG of length 219 |
| 25 | ID4144 | S | ORF starting with ATG of length 219 |
| | ID4145 | S | ORF starting with ATG of length 219 |
| | ID4146 | S | ORF starting with ATG of length 219 |
| | ID4147 | S | ORF starting with ATG of length 220 |
| | ID4148 | S | ORF starting with ATG of length 219 |
| 30 | ID4149 | S | ORF starting with ATG of length 219 |
| | ID4150 | S | ORF starting with ATG of length 219 |
| | ID4151 | S | ORF starting with ATG of length 218 |
| | ID4152 | S | COMX. |
| | ID4153 | S | ORF starting with ATG of length 216 |
| 35 | ID4154 | S | ORF starting with ATG of length 215 |
| | ID4155 | S | ORF starting with ATG of length 216 |
| | ID4156 | S | ORF starting with ATG of length 216 |
| | ID4157 | S | ORF starting with ATG of length 216 |
| | ID4158 | S | ORF starting with ATG of length 216 |
| 40 | ID4159 | S | ORF starting with ATG of length 216 |
| | ID4160 | S | Deduced protein sequence of p170-2 comprising T4. |
| | ID4161 | S | REGULATOR OF THE ACTIVITY OF PHOSPHATASE RAPK. |
| | ID4162 | S | M. tuberculosis SYNEC protein. |
| | ID4163 | S | ORF starting with ATG of length 216 |
| 45 | ID4164 | S | ORF starting with ATG of length 216 |
| | ID4165 | S | ORF starting with ATG of length 216 |
| | ID4166 | S | ORF starting with ATG of length 216 |
| | ID4167 | S | ORF starting with ATG of length 216 |
| | ID4168 | S | Streptococcus pneumoniae encoded polypeptide. |
| 50 | ID4169 | S | ORF starting with ATG of length 216 |
| | ID4170 | S | ORF starting with ATG of length 214 |
| | ID4171 | S | Nucleic acid transporter system peptide ligand SEQ ID NO 60. |
| | ID4172 | S | ORF starting with ATG of length 213 |
| 55 | ID4173 | S | ORF starting with TTG or GTG of length 426 |
| | ID4174 | S | ORF starting with ATG of length 212 |
| | ID4175 | S | ORF starting with ATG of length 213 |
| | ID4176 | S | ORF starting with ATG of length 213 |
| | ID4177 | S | ORF starting with ATG of length 213 |
| 60 | ID4178 | S | ORF starting with ATG of length 213 |
| | ID4179 | S | ORF starting with ATG of length 213 |
| | ID4180 | S | ORF starting with ATG of length 213 |
| | ID4181 | S | 90K-PROTEASE (BACILLOPEPTIDASE F) PRECURSOR |
| | (BACILLOPEPTIDAS | | |
| 65 | ID4182 | S | HYPOTHETICAL PROTEIN HI1600. |
| | ID4183 | S | ORF starting with ATG of length 213 |

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| | ID4184 | S | ORF starting with ATG of length 213 |
| | ID4185 | S | ORF starting with ATG of length 213 |
| | ID4186 | S | ORF starting with ATG of length 210 |
| | ID4187 | S | ORF starting with ATG of length 210 |
| 5 | ID4188 | S | ORF starting with ATG of length 210 |
| | ID4189 | S | ORF starting with ATG of length 210 |
| | ID4190 | S | ORF starting with ATG of length 210 |
| | ID4191 | S | ORF starting with ATG of length 210 |
| | ID4192 | S | ORF starting with ATG of length 210 |
| 10 | ID4193 | S | BH3511 PROTEIN. |
| | ID4194 | S | YISL PROTEIN. |
| | ID4195 | S | PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, F |
| | POLYPEPTIDE | P | |
| | ID4196 | S | ORF starting with ATG of length 207 |
| 15 | ID4197 | S | ORF starting with ATG of length 207 |
| | ID4198 | S | ORF starting with ATG of length 207 |
| | ID4199 | S | ORF starting with ATG of length 207 |
| | ID4200 | S | ORF starting with TTG or GTG of length 414 |
| | ID4201 | S | ORF starting with ATG of length 207 |
| 20 | ID4202 | S | ORF starting with ATG of length 207 |
| | ID4203 | S | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GNTR-HTPG |
| | INTERGEN | | |
| | ID4204 | S | PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN |
| | YQIY. | | |
| 25 | ID4205 | S | PHOSPHOTRANSACETYLASE. |
| | ID4206 | S | D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASE FAMILY. |
| | ID4207 | S | ORF starting with ATG of length 204 |
| | ID4208 | S | ORF starting with ATG of length 204 |
| | ID4209 | S | ORF starting with ATG of length 204 |
| 30 | ID4210 | S | BH3131 PROTEIN. |
| | ID4211 | S | Arabidopsis thaliana protein fragment SEQ ID NO: |
| | 22242. | | |
| | ID4212 | S | ORF starting with ATG of length 203 |
| | ID4213 | S | ORF starting with ATG of length 204 |
| 35 | ID4214 | S | ORF starting with ATG of length 204 |
| | ID4215 | S | ORF starting with ATG of length 204 |
| | ID4216 | S | ORF starting with ATG of length 204 |
| | ID4217 | S | ORF starting with ATG of length 205 |
| | ID4218 | S | RESPONSE REGULATOR PROTEIN (FRAGMENT) . |
| 40 | ID4219 | S | ORF starting with ATG of length 201 |
| | ID4220 | S | ORF starting with ATG of length 201 |
| | ID4221 | S | ORF starting with ATG of length 201 |
| | ID4222 | S | ORF starting with ATG of length 201 |
| | ID4223 | S | ORF starting with ATG of length 201 |
| 45 | ID4224 | S | ORF starting with ATG of length 201 |
| | ID4225 | S | ORF starting with ATG of length 201 |
| | ID4226 | S | ORF starting with ATG of length 201 |
| | ID4227 | S | ORF starting with ATG of length 201 |
| | ID4228 | S | ORF starting with TTG or GTG of length 402 |
| 50 | ID4229 | S | ORF starting with ATG of length 201 |
| | ID4230 | S | ORF starting with ATG of length 201 |
| | ID4231 | S | SPOIISA PROTEIN. |
| | ID4232 | S | YFIX. |
| | ID4233 | S | INTRACELLULAR ALKALINE PROTEASE. |
| 55 | ID4234 | S | STAGE V SPORULATION PROTEIN AA. |
| | ID4235 | S | YJZC PROTEIN. |
| | ID4236 | S | YFHO PROTEIN. |
| | ID4237 | T | PRKA PROTEIN. |
| | ID4238 | T | PUTATIVE SIGMA L-DEPENDENT TRANSCRIPTIONAL REGULATOR |
| 60 | IN MMGE | | |
| | ID4239 | T | HOMOLOGOUS TO SP:PHOR_BACSU. |
| | ID4240 | T | CARBON STARVATION PROTEIN A HOMOLOG. |
| | ID4241 | T | SPORULATION KINASE A (EC 2.7.3.-) (STAGE II |
| | SPORULATION | PROT | |
| 65 | ID4242 | T | YKRQ PROTEIN. |
| | ID4243 | T | PROBABLE SENSORY TRANSDUCTION HISTIDINE KINASE. |

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| | ID4244 | T | YVRG PROTEIN. |
| | ID4245 | T | YLAK PROTEIN. |
| | ID4246 | T | YKUI PROTEIN. |
| 5 | ID4247 | T | ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3.) |
| | ID4248 | T | SENSOR PROTEIN RESE (EC 2.7.3.-). |
| | ID4249 | T | YVQB PROTEIN. |
| | ID4250 | T | HOMOLOGUE OF ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN P |
| 10 | ID4251 | T | YKVD PROTEIN. |
| | ID4252 | T | AUTOLYSIN SENSOR KINASE. |
| | ID4253 | T | SUBTILIN BIOSYNTHESIS SENSOR PROTEIN SPAK (EC 2.7.3.-)) |
| 15 | ID4254 | T | HYPOTHETICAL 47.9 KDA PROTEIN IN DEGQ 5'REGION. |
| | ID4255 | T | HYPOTHETICAL 58.9 KDA PROTEIN. |
| | ID4256 | T | YTRP. |
| | ID4257 | T | YVQE PROTEIN. |
| | ID4258 | T | PUTATIVE SIGMA-B REGULATOR. |
| 20 | ID4259 | T | YLOP PROTEIN. |
| | ID4260 | T | SIGNAL TRANSDUCTION PROTEIN KINASE. |
| | ID4261 | T | FNR PROTEIN. |
| | ID4262 | T | HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE (EC 2.7.3.-) (ORFH) |
| 25 | ID4263 | T | CRP/FNR FAMILY PROTEIN. |
| | ID4264 | T | CITS (TWO-COMPONENT SENSOR HISTIDINE KINASE). |
| | ID4265 | T | YLBL PROTEIN. |
| | ID4266 | T | PROBABLE SERINE/THREONINE-PROTEIN KINASE IN SPOIIIE- HPT INTER |
| 30 | ID4267 | T | HYPOTHETICAL 35.7 KDA SENSORY TRANSDUCTION PROTEIN (ORFJ) (O) |
| | ID4268 | T | HYPOTHETICAL 42.3 KDA PROTEIN (YVFT PROTEIN). |
| | ID4269 | T | HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC |
| 35 | ID4270 | T | SENSOR PROTEIN DEGS (EC 2.7.3.-). |
| | ID4271 | T | ORF4 PROTEIN. |
| | ID4272 | T | GENERAL STRESS PROTEIN 16U (GSP16U). |
| | ID4273 | T | STRESS RESPONSE PROTEIN SCP2. |
| | ID4274 | T | HYPOTHETICAL 27.7 KDA PROTEIN (ORFQ). |
| 40 | ID4275 | T | CITS (TWO-COMPONENT SENSOR HISTIDINE KINASE). |
| | ID4276 | T | ORF starting with ATG of length 1569 |
| | ID4277 | T | ORF starting with ATG of length 1545 |
| | ID4278 | T | SIGNAL SENSOR PROTEIN HISTIDINE KINASE. |
| | ID4279 | T | BH2505 PROTEIN. |
| | ID4280 | T | PUTATIVE SIGMA-B REGULATOR. |
| 45 | ID4281 | T | HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC |
| | ID4282 | T | SENSOR PROTEIN. |
| | ID4283 | T | ORF starting with ATG of length 1233 |
| | ID4284 | T | ORF starting with ATG of length 1182 |
| 50 | ID4285 | T | ORF starting with ATG of length 1170 |
| | ID4286 | T | SPORULATION INITIATION PHOSPHOTRANSFERASE F (EC 2.7.- -.) (ST) |
| | ID4287 | T | ORF starting with ATG of length 1164 |
| | ID4288 | T | ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN |
| 55 | ID4289 | T | SPORULATION KINASE C (EC 2.7.3.-). |
| | ID4290 | T | ORF starting with ATG of length 1119 |
| | ID4291 | T | CHEMOTAXIS PROTEIN CHEY HOMOLOG. |
| | ID4292 | T | ORF starting with ATG of length 1083 |
| 60 | ID4293 | T | ANTI-SIGMA B FACTOR ANTAGONIST. |
| | ID4294 | T | YDCE PROTEIN. |
| | ID4295 | T | ANTI-SIGMA B FACTOR ANTAGONIST. |
| | ID4296 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE HOMOLOG. |
| | ID4297 | T | ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER). |
| 65 | ID4298 | T | YTAB PROTEIN. |

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| | ID4299 | T | PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE- |
| | PHOSPHATASE | Y | |
| | ID4300 | T | SPORULATION KINASE C (EC 2.7.3.-). |
| 5 | ID4301 | T | ORF starting with ATG of length 936 |
| | ID4302 | T | YJBP PROTEIN. |
| | ID4303 | T | HYPOTHETICAL 20.1 KDA PROTEIN. |
| | ID4304 | T | YBDM PROTEIN. |
| | ID4305 | T | YKOW PROTEIN. |
| | ID4306 | T | HYPOTHETICAL 20.3 KDA PROTEIN. |
| 10 | ID4307 | T | BH0415 PROTEIN. |
| | ID4308 | T | ORF starting with ATG of length 699 |
| | ID4309 | T | HYPOTHETICAL 40.7 KDA PROTEIN IN CSPB-GLPP INTERGENIC |
| | REGION | | |
| | ID4310 | T | ORF starting with ATG of length 1389 |
| 15 | ID4311 | T | YFKJ PROTEIN. |
| | ID4312 | T | ANTI-SIGMA F FACTOR (STAGE II SPORULATION PROTEIN |
| | AB). | | |
| | ID4313 | T | HYPOTHETICAL 31.8 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC | REGIO | |
| 20 | ID4314 | T | RECEPTOR-LIKE HISTIDINE KINASE BPDS. |
| | ID4315 | T | AUTOLYSIN SENSOR KINASE. |
| | ID4316 | T | YKOW PROTEIN. |
| | ID4317 | T | LYTS AND LYTR GENES, COMPLETE CDS. |
| 25 | ID4318 | T | BH2016 PROTEIN. |
| | ID4319 | T | ANTI-SIGMA F FACTOR (STAGE II SPORULATION PROTEIN |
| | AB). | | |
| | ID4320 | T | RESPONSE REGULATOR ACTA. |
| | ID4321 | T | ORF starting with ATG of length 1170 |
| 30 | ID4322 | T | ORF starting with ATG of length 780 |
| | ID4323 | T | ORF starting with ATG of length 255 |
| | ID4324 | T | ORF starting with ATG of length 249 |
| | ID4325 | T | ORF starting with ATG of length 239 |
| | ID4326 | T | CITS (TWO-COMPONENT SENSOR HISTIDINE KINASE). |
| 35 | ID4327 | T | YLAK PROTEIN. |
| | ID4328 | TK | STAGE II SPORULATION PROTEIN E (EC 3.1.3.16). |
| | ID4329 | TK | GTP PYROPHOSPHOKINASE (EC 2.7.6.5) (ATP:GTP 3'- |
| | PYROPHOSPHOTR | | |
| | ID4330 | TK | PUTATIVE SIGMA-B REGULATOR. |
| 40 | ID4331 | TK | Peptide which promotes formn. of B. subtilis |
| | extracellular p | | |
| | ID4332 | TK | SIGNAL TRANSDUCTION REGULATOR. |
| | ID4333 | TK | Streptococcus pneumoniae spo/rel protein sequence. |
| | ID4334 | TK | YVQA PROTEIN. |
| | ID4335 | TK | YVQC PROTEIN. |
| 45 | ID4336 | TK | VVRH PROTEIN (RECEIVER MODULE OF PUTATIVE RESPONSE |
| | REGULATOR | | |
| | ID4337 | TK | Staphylococcus aureus response regulator protein. |
| | ID4338 | TK | HYPOTHETICAL 27.5 KDA PROTEIN. |
| | ID4339 | TK | HYPOTHETICAL 27.2 KDA SENSORY TRANSDUCTION PROTEIN IN |
| 50 | ROCR-P | | |
| | ID4340 | TK | MTRA PROTEIN. |
| | ID4341 | TK | CITT (TWO-COMPONENT RESPONSE REGULATOR). |
| | ID4342 | TK | HYPOTHETICAL 22.8 KDA PROTEIN. |
| | ID4343 | TK | PHOSPHATE REGULATORY PROTEIN PHOB. |
| 55 | ID4344 | TK | HYPOTHETICAL 22.8 KDA PROTEIN. |
| | ID4345 | TK | VVRH PROTEIN (RECEIVER MODULE OF PUTATIVE RESPONSE |
| | REGULATOR | | |
| | ID4346 | TK | PUTATIVE TWO COMPONENT RESPONSE REGULATOR. |
| | ID4347 | TK | SCNR PROTEIN. |
| 60 | ID4348 | TK | ORF starting with ATG of length 615 |
| | ID4349 | TK | TWO-COMPONENT RESPONSE REGULATOR HOMOLOG. |
| | ID4350 | TK | ORF starting with ATG of length 506 |
| | ID4351 | TK | ORF starting with ATG of length 240 |
| | ID4352 | TK | ORF starting with ATG of length 228 |
| 65 | ID4353 | TQ | YUNI PROTEIN. |

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| | ID4354 | TQ | HYPOTHETICAL 47.8 KDA PROTEIN IN CAH-NASF INTERGENIC |
| | REGION | | |
| | ID4355 | TQ | ACETOIN UTILIZATION ACUC PROTEIN. |
| 5 | ID4356 | TQ | ORF starting with ATG of length 1614 |
| | ID4357 | TQ | ORF starting with ATG of length 1239 |
| | ID4358 | TQ | HYPOTHETICAL 47.8 KDA PROTEIN IN CAH-NASF INTERGENIC |
| | REGION | | |
| | ID4359 | TQ | ORF starting with ATG of length 942 |
| 10 | ID4360 | TQ | ORF starting with ATG of length 864 |
| | ID4361 | Z | transfer RNA-Ala |
| | ID4362 | Z | transfer RNA-Ile |
| | ID4363 | Z | transfer RNA-Ala |
| | ID4364 | Z | transfer RNA-Arg |
| 15 | ID4365 | Z | transfer RNA-Asn |
| | ID4366 | Z | transfer RNA-Asp |
| | ID4367 | Z | transfer RNA-Glu |
| | ID4368 | Z | transfer RNA-Gly |
| | ID4369 | Z | transfer RNA-Gly |
| 20 | ID4370 | Z | transfer RNA-His |
| | ID4371 | Z | transfer RNA-Ile |
| | ID4372 | Z | transfer RNA-Leu |
| | ID4373 | Z | transfer RNA-Leu |
| | ID4374 | Z | transfer RNA-Lys |
| 25 | ID4375 | Z | transfer RNA-Met |
| | ID4376 | Z | transfer RNA-Met |
| | ID4377 | Z | transfer RNA-Met |
| | ID4378 | Z | transfer RNA-Phe |
| | ID4379 | Z | transfer RNA-Pro |
| 30 | ID4380 | Z | transfer RNA-Ser |
| | ID4381 | Z | transfer RNA-Ser |
| | ID4382 | Z | transfer RNA-Thr |
| | ID4383 | Z | transfer RNA-Val |
| | ID4384 | Z | transfer RNA-Asn |
| 35 | ID4385 | Z | transfer RNA-Asp |
| | ID4386 | Z | transfer RNA-Gln |
| | ID4387 | Z | transfer RNA-Glu |
| | ID4388 | Z | transfer RNA-Gly |
| | ID4389 | Z | transfer RNA-His |
| 40 | ID4390 | Z | transfer RNA-Leu |
| | ID4391 | Z | transfer RNA-Leu |
| | ID4392 | Z | transfer RNA-Met |
| | ID4393 | Z | transfer RNA-Phe |
| | ID4394 | Z | transfer RNA-Ser |
| 45 | ID4395 | Z | transfer RNA-Thr |
| | ID4396 | Z | transfer RNA-Trp |
| | ID4397 | Z | transfer RNA-Tyr |
| | ID4398 | Z | transfer RNA-Val |
| | ID4399 | Z | transfer RNA-Arg |
| 50 | ID4400 | Z | transfer RNA-Asp |
| | ID4401 | Z | transfer RNA-Gly |
| | ID4402 | Z | transfer RNA-Met |
| | ID4403 | Z | transfer RNA-Ala |
| | ID4404 | Z | transfer RNA-Arg |
| 55 | ID4405 | Z | transfer RNA-Asn |
| | ID4406 | Z | transfer RNA-Gly |
| | ID4407 | Z | transfer RNA-Pro |
| | ID4408 | Z | transfer RNA-Thr |
| | ID4409 | Z | transfer RNA-Ala |
| 60 | ID4410 | Z | transfer RNA-Arg |
| | ID4411 | Z | transfer RNA-Gly |
| | ID4412 | Z | transfer RNA-Leu |
| | ID4413 | Z | transfer RNA-Leu |
| | ID4414 | Z | transfer RNA-Lys |
| | ID4415 | Z | transfer RNA-Pro |
| 65 | ID4416 | Z | transfer RNA-Thr |
| | ID4417 | Z | transfer RNA-Val |

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|----|--------|---|-------------------|
| | ID4418 | Z | transfer RNA-Ala |
| | ID4419 | Z | transfer RNA-Ile |
| | ID4420 | Z | transfer RNA-Arg |
| 5 | ID4421 | Z | transfer RNA-Asn |
| | ID4422 | Z | transfer RNA-Gln |
| | ID4423 | Z | transfer RNA-Glu |
| | ID4424 | Z | transfer RNA-Leu |
| | ID4425 | Z | transfer RNA-Leu |
| | ID4426 | Z | transfer RNA-Lys |
| 10 | ID4427 | Z | transfer RNA-Ser |
| | ID4428 | Z | transfer RNA-Ala |
| | ID4429 | Z | transfer RNA-Arg |
| | ID4430 | Z | transfer RNA-Arg |
| 15 | ID4431 | Z | transfer RNA-Gln |
| | ID4432 | Z | transfer RNA-Gln |
| | ID4433 | Z | transfer RNA-Glu |
| | ID4434 | Z | transfer RNA-Glu |
| | ID4435 | Z | transfer RNA-Gly |
| 20 | ID4436 | Z | transfer RNA-Met |
| | ID4437 | Z | transfer RNA-Ser |
| | ID4438 | Z | transfer RNA-Thr |
| | ID4439 | Z | transfer RNA-Tyr |
| | ID4440 | Z | transfer RNA-Val |
| 25 | ID4441 | Z | transfer RNA-Val |
| | ID4442 | Z | transfer RNA-Asp |
| | ID4443 | Z | transfer RNA-Glu |
| | ID4444 | Z | transfer RNA-Lys |
| | ID4445 | Z | transfer RNA-Phe |
| 30 | ID4446 | Z | ribosomal RNA-16S |
| | ID4447 | Z | ribosomal RNA-23S |
| | ID4448 | Z | ribosomal RNA-5S |

Appendix 2: *Bacillus clausii* annotation and divisions into functional categories**Information storage and processing**

5 J 1135-1295 Translation, ribosomal structure and biogenesis

K 1296-1472 Transcription

L 1473-1634 DNA replication, recombination and repair

10 **Cellular processes**

D 185-232 Cell division and chromosome partitioning

15 O 1816-1894 Posttranslational modification, protein turnover, chaperones

M 1635-1754 Cell envelope biogenesis, outer membrane

N 1755-1815 Cell motility and secretion

20 P 1895-2025 Inorganic ion transport and metabolism

T 3852-3947 Signal transduction mechanisms

25 **Metabolism**

C 1-184 Energy production and conversion

G 640-968 Carbohydrate transport and metabolism

30 E 233-544 Amino acid transport and metabolism

F 545-639 Nucleotide transport and metabolism

35 H 969-1067 Coenzyme metabolism

I 1068-1134 Lipid metabolism

Q 2026-2111 Secondary metabolites biosynthesis, transport and catabolism

40 **Structural RNA**

Z 3948-4033 tRNA and rRNA

45 **Functional category not assigned**

R 2212-2381 Functional category not assigned

S 2382-3851 Functional category not assigned

| | | | |
|----|-------------------|---|-------------------------------------------------------|
| 5 | ID0001 | C | NADH DEHYDROGENASE. |
| | ID0002 | C | ACONITATE HYDRATASE (EC 4.2.1.3) (CITRATE HYDRO- |
| | LYASE) (ACON | | |
| | ID0003 | C | L-LACTATE DEHYDROGENASE (EC 1.1.1.27). |
| | ID0004 | C | CYTOCHROME AA3 QUINOL OXIDASE SUBUNIT III (EC |
| | 1.10.3.). | | |
| 10 | ID0005 | C | CYTOCHROME AA3 QUINOL OXIDASE SUBUNIT I (EC 1.10.3.). |
| | ID0006 | C | QOXA (CYTOCHROME AA3 QUINOL OXIDASE SUBUNIT II) (EC |
| | 1.10.3.). | | |
| | ID0007 | C | MALATE SYNTHASE. |
| | ID0008 | C | ACETATE KINASE (EC 2.7.2.1) (ACETOKINASE). |
| 15 | ID0009 | C | ALCOHOL DEHYDROGENASE. |
| | ID0010 | C | L-lactic acid dehydrogenase. |
| | ID0011 | C | HYPOTHETICAL 35.0 KDA PROTEIN IN RAPJ-OPUAA |
| | INTERGENIC REGION | | |
| 20 | ID0012 | C | HYPOTHETICAL 49.3 KDA PROTEIN IN IDH-DEOR INTERGENIC |
| | REGION. | | |
| | ID0013 | C | PYRUVATE DEHYDROGENASE E2 (DIHYDROLIPOAMIDE |
| | ACETYLTRANSFERAS | | |
| | ID0014 | C | HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC |
| | REGION. | | |
| 25 | ID0015 | C | ACONITATE HYDRATASE (EC 4.2.1.3) (CITRATE HYDRO- |
| | LYASE) (ACON | | |
| | ID0016 | C | HYPOTHETICAL 49.3 KDA PROTEIN IN IDH-DEOR INTERGENIC |
| | REGION. | | |
| | ID0017 | C | ORF starting with ATG of length 558 |
| 30 | ID0018 | C | DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4) (E3 |
| | COMPONENT OF | | |
| | ID0019 | C | 68% IDENTITY PROTEIN TO 1-PYRROLINE-5-CARBOXYLATE |
| | DEHYDROGEN | | |
| | ID0020 | C | GLYCEROL KINASE. |
| 35 | ID0021 | C | ELECTRON TRANSFER FLAVOPROTEIN (BETA SUBUNIT). |
| | ID0022 | C | ALDEHYDE DEHYDROGENASE, THERMOSTABLE (EC 1.2.1.3). |
| | ID0023 | C | NADH DEHYDROGENASE. |
| | ID0024 | C | NADH DEHYDROGENASE-LIKE PROTEIN. |
| | ID0025 | C | Heat resistant aldehyde dehydrogenase. |
| 40 | ID0026 | C | GLYCOLATE OXIDASE SUBUNIT. |
| | ID0027 | C | ORF starting with ATG of length 351 |
| | ID0028 | C | MAGNESIUM CITRATE SECONDARY TRANSPORTER. |
| | ID0029 | C | Heat resistant aldehyde dehydrogenase. |
| | ID0030 | C | NITRITE REDUCTASE [NAD(P)H] (EC 1.6.6.4). |
| 45 | ID0031 | C | H(+) / SODIUM-GLUTAMATE SYMPORTER. |
| | ID0032 | C | PHOSPHOTRANSACETYLASE (EC 2.3.1.8). |
| | ID0033 | C | ORF starting with ATG of length 708 |
| | ID0034 | C | CITRATE SYNTHASE (EC 4.1.3.7). |
| | ID0035 | C | DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4) (E3 |
| 50 | COMPONENT OF | | |
| | ID0036 | C | BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE E1. |
| | ID0037 | C | OXIDOREDUCTASE. |
| | ID0038 | C | GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL 3- |
| | PHOSPHOTRANSFE | | |
| 55 | ID0039 | C | ATP SYNTHASE ALPHA SUBUNIT (EC 3.6.1.34). |
| | ID0040 | C | ISOCITRATE LYASE. |
| | ID0041 | C | Amino acid sequence of respiratory Nitrate Reductase |
| | 1 alpha | | |
| | ID0042 | C | Staphylococcus aureus respiratory nitrate reductase |
| 60 | alpha su | | |
| | ID0043 | C | PTS SYSTEM, MANNITOL-SPECIFIC ENZYME II, BC |
| | COMPONENT. | | |

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|----|----------|---|----------------------------------------------------------------|
| | ID0044 | C | Staphylococcus carnosus nitrate reductase biogenesis protein |
| | ID0045 | C | PUTATIVE PROTON-TRANSLOCATING ATPASE, BETA SUBUNIT (EC 3.6.1) |
| 5 | ID0046 | C | PUTATIVE NITRATE REDUCTASE ALPHA CHAIN. |
| | ID0047 | C | ATP SYNTHASE BETA SUBUNIT (EC 3.6.1.34). |
| | ID0048 | C | ASSIMILATORY NITRATE REDUCTASE CATALYTIC SUBUNIT (EC 1.7.99.) |
| 10 | ID0049 | C | ORF starting with ATG of length 918 |
| | ID0050 | C | ASSIMILATORY NITRATE REDUCTASE CATALYTIC SUBUNIT (EC 1.7.99.) |
| | ID0051 | C | GLYCOLATE OXIDASE SUBUNIT. |
| | ID0052 | C | L-lactic acid dehydrogenase. |
| 15 | ID0053 | C | GLYCOLATE OXIDASE SUBUNIT. |
| | ID0054 | C | HYPOTHETICAL 49.2 KDA PROTEIN. |
| | ID0055 | C | PROBABLE METHYLMALONATE-SEMALDEHYDE DEHYDROGENASE [ACYLATIN] |
| | ID0056 | C | GLYCOLATE OXIDASE IRON-SULFUR SUBUNIT. |
| 20 | ID0057 | C | ALDO/KETO REDUCTASE. |
| | ID0058 | C | NA(+)/H(+) ANTIPORTER (SODIUM/PROTON ANTIPORTER). |
| | ID0059 | C | MALIC ENZYME (MALATE DEHYDROGENASE) (EC 1.1.1.38). |
| | ID0060 | C | HYPOTHETICAL 48.5 KDA PROTEIN. |
| | ID0061 | C | PROBABLE D-LACTATE DEHYDROGENASE. |
| 25 | ID0062 | C | PROBABLE METHYLMALONATE-SEMALDEHYDE DEHYDROGENASE [ACYLATIN] |
| | ID0063 | C | GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5). |
| | ID0064 | C | GLYCEROL-3-PHOSPHATE DEHYDROGENASE. |
| | ID0065 | C | ALKANESULFONATE MONOOXYGENASE. |
| 30 | ID0066 | C | GLYCEROL-3-PHOSPHATE DEHYDROGENASE. |
| | ID0067 | C | GLYCOLATE OXIDASE IRON-SULFUR SUBUNIT. |
| | ID0068 | C | MALATE SYNTHASE. |
| | ID0069 | C | CITRATE SYNTHASE III (EC 4.1.3.7). |
| | ID0070 | C | BH1020 PROTEIN. |
| 35 | ID0071 | C | METHYLMALONATE-SEMALDEHYDE DEHYDROGENASE. |
| | ID0072 | C | METHYLMALONATE-SEMALDEHYDE DEHYDROGENASE. |
| | ID0073 | C | OMEGA-CRYSTALLIN. |
| | ID0074 | C | L-LACTATE PERMEASE. |
| | ID0075 | C | GLYCOLATE OXIDASE. |
| 40 | ID0076 | C | BH1833 PROTEIN. |
| | ID0077 | C | HYPOTHETICAL 49.2 KDA PROTEIN. |
| | ID0078 | C | GLYCEROL KINASE. |
| | ID0079 | C | ATP SYNTHASE B SUBUNIT (EC 3.6.1.34). |
| | ID0080 | C | SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT. |
| 45 | ID0081 | C | NADH DEHYDROGENASE. |
| | ID0082 | C | HYPOTHETICAL 47.8 KDA PROTEIN. |
| | ID0083 | C | PYRUVATE DEHYDROGENASE E2 (DIHYDROLIPOAMIDE ACETYLTRANSFERASE) |
| | ID0084 | C | DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4) (E3 COMPONENT OF |
| 50 | ID0085 | C | PROBABLE ALDEHYDE DEHYDROGENASE YCBD (EC 1.2.1.3). |
| | ID0086 | C | PROBABLE FLAVODOXIN 1. |
| | ID0087 | C | HYPOTHETICAL 79.2 KDA PROTEIN IN ACDA 5'REGION. |
| | ID0088 | C | ORF starting with ATG of length 969 |
| | ID0089 | C | TPP-DEPENDENT ACETOIN DEHYDROGENASE, E1 ALPHA- |
| 55 | SUBUNIT. | | GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE. |
| | ID0090 | C | ATP SYNTHASE ALPHA SUBUNIT (EC 3.6.1.34). |
| | ID0091 | C | Staphylococcus aureus respiratory nitrate reductase alpha su |
| 60 | ID0093 | C | MANGANESE-DEPENDENT INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (P) |
| | ID0094 | C | PROBABLE NADH-DEPENDENT BUTANOL DEHYDROGENASE 1 (EC 1.1.1.-) |
| | ID0095 | C | MALATE DEHYDROGENASE (EC 1.1.1.37). |
| 65 | ID0096 | C | ASSIMILATORY NITRITE REDUCTASE (SUBUNIT). |
| | ID0097 | C | ISOCITRATE DEHYDROGENASE (EC 1.1.1.42). |

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| | ID0098 | C | NITRATE REDUCTASE (FRAGMENT). |
| | ID0099 | C | ASSIMILATORY NITRITE REDUCTASE (SUBUNIT). |
| | ID0100 | C | ALDEHYDE DEHYDROGENASE, THERMOSTABLE (EC 1.2.1.3). |
| 5 | ID0101 | C | BH0875 PROTEIN. |
| | ID0102 | C | ALDEHYDE DEHYDROGENASE. |
| | ID0103 | C | SUCCINATE-SEMALDEHYDE DEHYDROGENASE. |
| | ID0104 | C | HYDA (FRAGMENT). |
| | ID0105 | C | PROBABLE ALDEHYDE DEHYDROGENASE YCBD (EC 1.2.1.3). |
| 10 | ID0106 | C | PTS SYSTEM, MANNITOL-SPECIFIC ENZYME II, BC |
| | COMPONENT. | | |
| | ID0107 | C | PROBABLE ALDEHYDE DEHYDROGENASE YWDH (EC 1.2.1.3). |
| | ID0108 | C | ATP SYNTHASE SUBUNIT C (EC 3.6.1.34). |
| | ID0109 | C | ATP SYNTHASE A SUBUNIT (EC 3.6.1.34). |
| 15 | ID0110 | C | NADP-DEPENDENT ALDEHYDE DEHYDROGENASE (EC 1.2.1.3). |
| | ID0111 | C | L-ARABINOSE UTILIZATION PROTEIN. |
| | ID0112 | C | PROBABLE ALDEHYDE DEHYDROGENASE YCBD (EC 1.2.1.3). |
| | ID0113 | C | L-RIBULOKINASE. |
| | ID0114 | C | L-ARABINOSE UTILIZATION PROTEIN. |
| 20 | ID0115 | C | ALDEHYDE DEHYDROGENASE, THERMOSTABLE (EC 1.2.1.3). |
| | ID0116 | C | CYTOCHROME CAA3 OXIDASE (SUBUNIT I). |
| | ID0117 | C | GLYCEROL-3-PHOSPHATE DEHYDROGENASE. |
| | ID0118 | C | GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5). |
| | ID0119 | C | OXOGLUTARATE DEHYDROGENASE. |
| 25 | ID0120 | C | PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31) |
| | (PEPCASE) | (PEP | |
| | ID0121 | C | PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31) |
| | (PEPCASE) | (PEP | |
| | ID0122 | C | NADPH-FLAVIN OXIDOREDUCTASE. |
| 30 | ID0123 | C | Protein encoded by <i>C. trachomatis</i> LGV II clone 4C9-18 |
| | # 2. | | |
| | ID0124 | C | <i>Staphylococcus carnosus</i> nitrate reductase NarJ |
| | subunit. | | |
| | ID0125 | C | HYPOTHETICAL OXIDOREDUCTASE IN CSTA-AHPC INTERGENIC |
| | REGION. | | |
| 35 | ID0126 | C | PROBABLE NADH-DEPENDENT BUTANOL DEHYDROGENASE 1 (EC |
| | 1.1.1.-) | | |
| | ID0127 | C | MG++/CITRATE COMPLEX TRANSPORTER. |
| | ID0128 | C | MALATE SYNTHASE. |
| 40 | ID0129 | C | SUCCINATE DEHYDROGENASE FLAVOPROTEIN (EC 1.3.99.1). |
| | ID0130 | C | MALIC ENZYME (MALATE DEHYDROGENASE) (EC 1.1.1.38). |
| | ID0131 | C | SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC |
| | 1.3.99.1). | | |
| | ID0132 | C | 1.1.1.38). |
| 45 | ID0133 | C | MALATE OXIDOREDUCTASE (NAD) (MALIC ENZYME) (EC |
| | ID0134 | C | FUMARATE HYDRATASE. |
| | ID0135 | C | NAD-DEPENDENT METHANOL DEHYDROGENASE. |
| | ID0136 | C | SUCCINYL-COA SYNTHETASE (ALPHA SUBUNIT). |
| | ID0137 | C | NADH-DEPENDENT FLAVIN OXIDOREDUCTASE, PUTATIVE. |
| 50 | ID0138 | C | CYTOCHROME CAA3 OXIDASE (SUBUNIT III). |
| | ID0139 | C | CYTOCHROME CAA3 OXIDASE (SUBUNIT IV). |
| | ID0140 | C | GLYCEROL DEHYDROGENASE (EC 1.1.1.6) (GLDH). |
| | ID0141 | C | ALDEHYDE DEHYDROGENASE. |
| | ID0142 | C | ORF starting with ATG of length 942 |
| 55 | ID0143 | C | CYTOCHROME AA3 QUINOL OXIDASE SUBUNIT I (EC 1.10.3.). |
| | ID0144 | C | CYTOCHROME AA3 QUINOL OXIDASE SUBUNIT II (EC |
| | 1.10.3.). | | |
| | ID0145 | C | ASSIMILATORY NITRATE REDUCTASE CATALYTIC SUBUNIT (EC |
| 60 | ID0146 | C | 1.7.99. |
| | ID0146 | C | RIESKE. |
| | ID0147 | C | PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT (EC |
| | ID0148 | C | 1.2.4. |
| | ID0149 | C | SUCCINYL-COA SYNTHETASE (BETA SUBUNIT). |
| 65 | BETA SUBUN | | BH1718 PROTEIN. |
| | ID0150 | C | ACETOIN DEHYDROGENASE E1 COMPONENT (TPP-DEPENDENT |
| | | | HYPOTHETICAL 47.8 KDA PROTEIN. |

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| | | | CITRATE PERMEASE/TRANSPORTER. |
| | | C | PUTATIVE MALATE OXIDOREDUCTASE. |
| | | C | ALDEHYDE DEHYDROGENASE, THERMOSTABLE (EC 1.2.1.3). |
| | | C | MAGNESIUM CITRATE SECONDARY TRANSPORTER. |
| 5 | ID0155 | C | DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTA |
| | ID0156 | C | FERREDOXIN. |
| | ID0157 | C | ACETOIN DEHYDROGENASE E2 COMPONENT (DIHYDROLIPOAMIDEACETYLTR |
| 10 | ID0158 | C | OXIDOREDUCTASE, N5,N10-METHYLENETETRAHYDROMETHANOPTERIN REDU |
| | ID0159 | C | PROBABLE ALDEHYDE DEHYDROGENASE YCBD (EC 1.2.1.3). |
| | ID0160 | C | CITRATE TRANSPORTER. |
| | ID0161 | C | GLYCOLATE OXIDASE SUBUNIT. |
| 15 | ID0162 | C | BH3449 PROTEIN. |
| | ID0163 | C | PYRUVATE CARBOXYLASE. |
| | ID0164 | C | SULFONATE MONOOXYGENASE. |
| | ID0165 | C | ORF starting with ATG of length 702 |
| 20 | ID0166 | C | ATP SYNTHASE GAMMA SUBUNIT (EC 3.6.1.34). |
| | ID0167 | C | ATP SYNTHASE ALPHA SUBUNIT (EC 3.6.1.34). |
| | ID0168 | C | ATP SYNTHASE DELTA SUBUNIT (EC 3.6.1.34). |
| | ID0169 | C | ATP SYNTHASE B SUBUNIT (EC 3.6.1.34). |
| | ID0170 | C | GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE. |
| | ID0171 | C | GLYCOLATE OXIDASE IRON-SULFUR SUBUNIT. |
| 25 | ID0172 | C | METHYLMALONATE-SEMALDEHYDE DEHYDROGENASE. |
| | ID0173 | C | BH0303 PROTEIN. |
| | ID0174 | C | ASSIMILATORY NITRITE REDUCTASE (SUBUNIT). |
| | ID0175 | C | ALDEHYDE DEHYDROGENASE, THERMOSTABLE (EC 1.2.1.3). |
| | ID0176 | C | PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT (EC |
| 30 | 1.2.4. | | |
| | ID0177 | CHR | YVCT PROTEIN. |
| | ID0178 | CP | ORF1 (NA+/H+ ANTIPORTER). |
| | ID0179 | CP | MULTIPLE RESISTANCE AND PH REGULATION RELATED PROTEIN |
| | A. | | |
| 35 | ID0180 | CP | NADH DEHYDROGENASE, PUTATIVE. |
| | ID0181 | CP | ORF1 (NA+/H+ ANTIPORTER). |
| | ID0182 | CP | YUFT PROTEIN. |
| | ID0183 | CP | NA+/H+ ANTIPORTER. |
| | ID0184 | CR | ORF starting with ATG of length 626 |
| 40 | ID0185 | D | SEPTUM SITE-DETERMINING PROTEIN. |
| | ID0186 | D | CELL-SHAPE DETERMINING PROTEIN. |
| | ID0187 | D | BH0975 PROTEIN. |
| | ID0188 | D | HYPOTHETICAL 53.5 KDA PROTEIN IN SPOIIIE-HPT |
| | INTERGENIC REGIO | | |
| 45 | ID0189 | D | YUKA PROTEIN. |
| | ID0190 | D | CENTROMERE-LIKE FUNCTION INVOLVED IN FORESPORE |
| | CHROMOSOME PA | | |
| | ID0191 | D | CELL SHAPE DETERMINING PROTEIN (MREB-LIKE PROTEIN). |
| | ID0192 | D | CELL-CYCLE PROTEIN. |
| 50 | ID0193 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0194 | D | SPOIIIE PROTEIN. |
| | ID0195 | D | SPORULATION PROTEIN SPOIIIE. |
| | ID0196 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0197 | D | GLUCOSE INHIBITED DIVISION PROTEIN A. |
| 55 | ID0198 | D | BH0975 PROTEIN. |
| | ID0199 | D | SCDA. |
| | ID0200 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0201 | D | CELL-SHAPE DETERMINING PROTEIN. |
| | ID0202 | D | CELL-SHAPE DETERMINING PROTEIN. |
| 60 | ID0203 | D | CAPSULAR POLYSACCHARIDE BIOSYNTHESIS. |
| | ID0204 | D | SPOIIIE PROTEIN. |
| | ID0205 | D | SA0276 PROTEIN. |
| | ID0206 | D | BH0975 PROTEIN. |
| | ID0207 | D | DIARRHEAL TOXIN. |
| 65 | ID0208 | D | ORF starting with ATG of length 351 |
| | ID0209 | D | ORF starting with ATG of length 1014 |

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| | ID0210 | D | CHROMOSOME PARTITION PROTEIN SMC. |
| | ID0211 | D | GLUCOSE-INHIBITED DIVISION PROTEIN. |
| | ID0212 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0213 | D | CELL-SHAPE DETERMINING PROTEIN. |
| 5 | ID0214 | D | LATENT NUCLEAR ANTIGEN. |
| | ID0215 | D | CELL-DIVISION INITIATION PROTEIN (SEPTUM PLACEMENT). |
| | ID0216 | D | CELL-DIVISION INITIATION PROTEIN (SEPTUM FORMATION). |
| | ID0217 | D | CELL-DIVISION PROTEIN (SEPTUM FORMATION). |
| | ID0218 | D | CELL-DIVISION PROTEIN (SEPTUM FORMATION). |
| 10 | ID0219 | D | CHROMOSOME SEGREGATION SMC PROTEIN. |
| | ID0220 | D | STAGE II SPORULATION PROTEIN D. |
| | ID0221 | D | CELL SHAPE DETERMINING PROTEIN (MREB-LIKE PROTEIN). |
| | ID0222 | D | GLUCOSE INHIBITED DIVISION PROTEIN A. |
| | ID0223 | D | ATP-BINDING MRP PROTEIN (MRP/NBP35 FAMILY). |
| 15 | ID0224 | D | STAGE V SPORULATION PROTEIN E (REQUIRED FOR SPORE |
| | CORTEX SYN | | |
| | ID0225 | D | DNA TRANSLOCASE (STAGE III SPORULATION PROTEIN |
| | SPOIIIE). | | |
| | ID0226 | D | GLUCOSE-INHIBITED DIVISION PROTEIN. |
| 20 | ID0227 | D | CENTROMERE-LIKE FUNCTION INVOLVED IN FORESPORE |
| | CHROMOSOME PA | | |
| | ID0228 | D | GLUCOSE-INHIBITED DIVISION PROTEIN. |
| | ID0229 | D | SPOIIIE PROTEIN. |
| | ID0230 | D | Amino acid sequence of a <i>Chlamydia trachomatis</i> |
| 25 | protein. | | |
| | ID0231 | D | STAGE V SPORULATION PROTEIN E. |
| | ID0232 | D | 186AA LONG HYPOTHETICAL MAF PROTEIN. |
| | ID0233 | E | CYSTATHIONINE GAMMA-SYNTHASE (O-SUCCINYLHOMOSERINE |
| | (THIOL) -L | | |
| 30 | ID0234 | E | SA1216 PROTEIN. |
| | ID0235 | E | RIESKE. |
| | ID0236 | E | CEPHALOSPORIN ACYLASE. |
| | ID0237 | E | DIAMINOPIMELATE DECARBOXYLASE. |
| | ID0238 | E | 5-METHYLtetrahydrofolate S-HOMOCYSTEINE |
| 35 | METHYLTRANSFERASE (EC | | |
| | ID0239 | E | TRYPTOPHAN SYNTHASE (ALPHA SUBUNIT). |
| | ID0240 | E | HOMOSYSTEIN METHYL TRANSFERASE. |
| | ID0241 | E | GLUTAMATE SYNTHASE (LARGE SUBUNIT). |
| | ID0242 | E | TRYPTOPHAN SYNTHASE (BETA SUBUNIT). |
| 40 | ID0243 | E | PHOSPHORIBOSYL ANTHRANILATE ISOMERASE. |
| | ID0244 | E | HOMOCITRATE SYNTHASE. |
| | ID0245 | E | HOMOSYSTEIN METHYL TRANSFERASE. |
| | ID0246 | E | ORF starting with ATG of length 417 |
| | ID0247 | E | PROLINE OXIDASE (PROLINE DEHYDROGENASE). |
| 45 | ID0248 | E | ASPARAGINE SYNTHETASE. |
| | ID0249 | E | GAMMA-GLUTAMYL KINASE. |
| | ID0250 | E | L-CYSTEINE SULFURTRANSFERASE (IRON-SULFUR COFACTOR |
| | SYNTHESIS | | |
| | ID0251 | E | AMINOTRANSFERASE REQUIRED FOR NAD BIOSYNTHESIS (NIFS |
| 50 | PROTEIN | | |
| | ID0252 | E | HYPOTHETICAL 38.3 KDA PROTEIN IN PEPT-KATB INTERGENIC |
| | REGION | | |
| | ID0253 | E | ORF starting with ATG of length 357 |
| | ID0254 | E | AROMATIC AMINO ACID TRANSPORTER. |
| 55 | ID0255 | E | FE-S CLUSTER FORMATION PROTEIN. |
| | ID0256 | E | GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ. |
| | ID0257 | E | UROCANATE HYDRATASE. |
| | ID0258 | E | PROBABLE AMINOTRANSFERASE IN KATA 3' REGION (EC 2.6.- |
| | .-) (ORF | | |
| 60 | ID0259 | E | DPPA. |
| | ID0260 | E | TETRAHYDRODIPICOLINATE SUCCINYLASE. |
| | ID0261 | E | ARGININOSUCCINATE SYNTHASE (CITRULLINE-ASPARATE |
| | LIGASE) (EC | | |
| | ID0262 | E | INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48) |
| 65 | (IGPS). | | |
| | ID0263 | E | SA0678 PROTEIN. |

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| | ID0264 | E | HOMOSERINE DEHYDROGENASE (EC 1.1.1.3). |
| | ID0265 | E | LYSINE-SPECIFIC PERMEASE. |
| | ID0266 | E | BH0591 PROTEIN. |
| | ID0267 | E | PREPHENATE DEHYDROGENASE. |
| 5 | ID0268 (IMIDAZOL | E | HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) |
| | ID0269 | E | HYPOTHETICAL 34.8 KDA PROTEIN PH1048. |
| | ID0270 | E | O-ACETYLHOMOSERINE SULFHYDRYLASE. |
| 10 | ID0271 8020. | E | Arabidopsis thaliana protein fragment SEQ ID NO: |
| | ID0272 | E | PROLINE OXIDASE (PROLINE DEHYDROGENASE). |
| | ID0273 | E | FOSFOMYCIN RESISTANCE PROTEIN. |
| | ID0274 | E | Corynebacterium glutamicum MP protein sequence SEQ ID |
| | NO:338 | | |
| 15 | ID0275 | E | ARGININOSUCCINATE LYASE (EC 4.3.2.1). |
| | ID0276 | E | HOMOSERINE KINASE (EC 2.7.1.39). |
| | ID0277 | E | ASPARTATE AMINOTRANSFERASE. |
| | ID0278 | E | PROBABLE CYSTEINE SYNTHASE (EC 4.2.99.8) (O- |
| 20 | ACETYLSERINESULF | | |
| | ID0279 | E | GLYCINE DEHYDROGENASE SUBUNIT 1. |
| | ID0280 | E | PROLINE DEHYDROGENASE. |
| | ID0281 | E | SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT). |
| | ID0282 | E | LYSINE DECARBOXYLASE. |
| | ID0283 | E | YLMB PROTEIN. |
| 25 | ID0284 | E | GLYCINE DEHYDROGENASE SUBUNIT 2. |
| | ID0285 | E | PROBABLE GLYCINE DEHYDROGENASE [DECARBOXYLATING] |
| | SUBUNIT 1(E | | |
| | ID0286 | E | BH3148 PROTEIN. |
| 30 | OXO-ACI | | |
| | ID0287 | E | ORNITHINE AMINOTRANSFERASE (EC 2.6.1.13) (ORNITHINE-- |
| | ID0288 | E | HYPOTHETICAL CYCLODEAMINASE Y4TK (EC 4.3.1.-). |
| | ID0289 | E | PEPTIDASE T (EC 3.4.11.-) (AMINOTRIPEPTIDASE) |
| | (TRIPEPTIDASE) | | |
| 35 | ID0290 | E | ORF starting with ATG of length 1224 |
| | ID0291 | E | YURW PROTEIN. |
| | ID0292 | E | HYDANTOINASE. |
| | ID0293 | E | 3-DEHYDROQUINATE SYNTHASE. |
| | ID0294 | E | S. pneumoniae phospho-2-dehydro-3-deoxyheptonate |
| | aldolase. | | |
| 40 | ID0295 | E | CHORISMATE SYNTHASE (EC 4.6.1.4) (5- |
| | ENOLPYRUVYLSHIKIMATE-3-P | | |
| | ID0296 | E | BH1779 PROTEIN. |
| | ID0297 | E | UROCANATE HYDRATASE. |
| | ID0298 | E | TRANSCRIPTIONAL REGULATOR OF ARGININE METABOLISM |
| 45 | EXPRESSION. | | |
| | ID0299 | E | HYPOTHETICAL 63.8 KDA PROTEIN IN SIPU-PBPC INTERGENIC |
| | REGION | | |
| | ID0300 | E | AMINOMETHYLTRANSFERASE. |
| | ID0301 | E | PUTATIVE THREONINE DEHYDRATASE (EC 4.2.1.16) |
| 50 | (THREONINE DEAM | | |
| | ID0302 | E | BH2170 PROTEIN. |
| | ID0303 | E | AROMATIC AMINO ACID TRANSPORTER. |
| | ID0304 | E | GLUTAMATE SYNTHASE (LARGE SUBUNIT). |
| | ID0305 | E | AROMATIC AMINO ACID TRANSPORTER. |
| 55 | ID0306 | E | AMINOTRANSFERASE. |
| | ID0307 | E | 0 DAY NEONATE SKIN CDNA, RIKEN FULL-LENGTH ENRICHED |
| | LIBRARY, | | |
| | ID0308 | E | DIAMINOBUTYRIC ACID AMINOTRANSFERASE. |
| | ID0309 | E | L-SERINE DEHYDRATASE BETA SUBUNIT. |
| 60 | ID0310 | E | L-SERINE DEHYDRATASE ALPHA SUBUNIT. |
| | ID0311 | E | BH0606 PROTEIN. |
| | ID0312 | E | TRYPTOPHAN 2,3-DIOXYGENASE, PUTATIVE. |
| | ID0313 | E | XAA-PRO DIPEPTIDASE. |
| | ID0314 | E | CYSTEINE SYNTHASE A (EC 4.2.99.8). |
| 65 | ID0315 | E | PROBABLE PERMEASE OF ABC TRANSPORTER. |
| | ID0316 | E | SA1675 PROTEIN. |

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| | ID0317 | E | HIGH-AFFINITY PERIPLASMIC GLUTAMINE BINDING PROTEIN. |
| | ID0318 | E | ORF starting with ATG of length 1137 |
| | ID0319 | E | GLYCINE BETAINE TRANSPORT SYSTEM PERMEASE PROTEIN. |
| 5 | ID0320 | E | ORF starting with ATG of length 499 |
| | ID0321 | E | SHIKIMATE 5-DEHYDROGENASE. |
| | ID0322 | E | ARGININOSUCCINATE LYASE (EC 4.3.2.1) |
| | (ARGINOSUCCINASE) (ASAL | | |
| | ID0323 | E | PROLIDASE (PROLINE DIPEPTIDASE) (EC 3.4.13.9). |
| 10 | ID0324 | E | LEUCINE DEHYDROGENASE (EC 1.4.1.9) (LEUDH). |
| | ID0325 | E | ATPASE HOMOLOG GBUA. |
| | ID0326 | E | CYSTEINE SYNTHASE. |
| | ID0327 | E | BH3306 PROTEIN. |
| | ID0328 | E | OLIGOENDOPEPTIDASE F. |
| | ID0329 | E | BH1629 PROTEIN. |
| 15 | ID0330 | E | 5-METHYLTETRAHYDROFOLATE S-HOMOCYSTEINE |
| | METHYLTRANSFERASE (EC | | |
| | ID0331 | E | BH1629 PROTEIN. |
| | ID0332 | E | BH0654 PROTEIN. |
| | ID0333 | E | LYSINE DECARBOXYLASE. |
| 20 | ID0334 | E | GLYCINE BETAINE-BINDING PROTEIN PRECURSOR. |
| | ID0335 | E | BH1629 PROTEIN. |
| | ID0336 | E | ORF starting with ATG of length 525 |
| | ID0337 | E | GLUTAMINE ABC TRANSPORTER (GLUTAMINE-BINDING |
| | PROTEIN). | | |
| 25 | ID0338 | E | LYSINE DECARBOXYLASE. |
| | ID0339 | E | GLUTAMINE ABC TRANSPORTER (INTEGRAL MEMBRANE |
| | PROTEIN). | | |
| | ID0340 | E | GLUTAMINE ABC TRANSPORTER (INTEGRAL MEMBRANE |
| | PROTEIN). | | |
| 30 | ID0341 | E | ORF starting with ATG of length 492 |
| | ID0342 | E | GLUTAMINE SYNTHETASE. |
| | ID0343 | E | CYSS. |
| | ID0344 | E | CYSTEINE SYNTHASE. |
| | ID0345 | E | ORF starting with ATG of length 240 |
| 35 | ID0346 | E | CYSTATHIONINE GAMMA-LYASE. |
| | ID0347 | E | HYPOTHETICAL 39.7 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| | REGION | | |
| | ID0348 | E | ASPARTATE AMMONIA-LYASE. |
| | ID0349 | E | 5-METHYLTETRAHYDROFOLATE S-HOMOCYSTEINE |
| 40 | METHYLTRANSFERASE (EC | | |
| | ID0350 | E | ALANINE DEHYDROGENASE (STAGE V SPORULATION PROTEIN N) |
| | (EC 1. | | |
| | ID0351 | E | GLUTAMINE SYNTHETASE. |
| | ID0352 | E | GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (EC |
| 45 | 6.3.1.2 | | |
| | ID0353 | E | T. vaginalis homocysteinase # 2. |
| | ID0354 | E | BH0774 PROTEIN. |
| | ID0355 | E | XAA-PRO DIPEPTIDASE. |
| | ID0356 | E | CYSTATHIONINE GAMMA-LYASE. |
| 50 | ID0357 | E | NON-ESSENTIAL GENE FOR COMPETENCE (PYRROLINE-5- |
| | CARBOXYLATE R | | |
| | ID0358 | E | MLR3804 PROTEIN. |
| | ID0359 | E | THERMOSTABLE DIPEPTIDASE BDP. |
| | ID0360 | E | N-CARBAMOYL-L-AMINO ACID AMIDOHYDROLASE (AMAB) (EC |
| 55 | 3.5.1.). | | |
| | ID0361 | E | THREONINE DEHYDRATASE. |
| | ID0362 | E | MLR3804 PROTEIN. |
| | ID0363 | E | NAD BIOSYNTHESIS. |
| | ID0364 | E | 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTTRANSFERASE. |
| 60 | ID0365 | E | GLUTAMATE DEHYDROGENASE. |
| | ID0366 | E | PREPHENATE DEHYDRATASE. |
| | ID0367 | E | N-CARBAMOYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.-) |
| | (L-CARB | | |
| | ID0368 | E | 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTTRANSFERASE. |
| 65 | ID0369 | E | HYPOTHETICAL 39.4 KDA OXIDOREDUCTASE IN HOM-MRGA |
| | INTERGENIC | | |

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| | ID0370 | E | PROBABLE D-SERINE DEHYDRATASE (EC 4.2.1.14) (D-SERINE DEAMIN |
| | ID0371 | E | SERINE DEAMINASE (FRAGMENT). |
| | ID0372 | E | ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18). |
| 5 | ID0373 | E | HISTIDINOL DEHYDROGENASE (EC 1.1.1.23). |
| | ID0374 | E | ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17). |
| | ID0375 | E | N-ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11). |
| | ID0376 | E | GLYCINE BETAINE/CARNITINE/CHOLINE ABC TRANSPORTER (ATP-BINDI |
| 10 | ID0377 | E | ACETYLORNITHINE DEACETYLASE (EC 3.5.1.16) (ACETYLORNITHINASE |
| | ID0378 | E | ORF starting with ATG of length 778 |
| | ID0379 | E | GLYCINE DEHYDROGENASE SUBUNIT 2. |
| | ID0380 | E | SA0677 PROTEIN. |
| 15 | ID0381 | E | CHOLINE ABC TRANSPORTER ATP BINDING PROTEIN. |
| | ID0382 | E | ARGININOSUCCINATE LYASE. |
| | ID0383 | E | PUTATIVE GLYCINE-BETAINE BINDING PERMEASE PROTEIN. |
| | ID0384 | E | ORF starting with ATG of length 564 |
| 20 | ID0385 | E | 3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85). |
| | ID0386 | E | DEF-6 PROTEIN. |
| | ID0387 | E | YUSX PROTEIN. |
| | ID0388 | E | 3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33). |
| 25 | ID0389 | E | 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33). |
| | ID0390 | E | PROBABLE PEPTIDASE YUXL (EC 3.4.21.-). |
| | ID0391 | E | ORF starting with ATG of length 612 |
| | ID0392 | E | PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTID |
| 30 | ID0393 | E | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0394 | E | PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN YCKA. |
| | ID0395 | E | PROBABLE ABC TRANSPORTER EXTRACELLULAR BINDING PROTEIN YCKB |
| 35 | ID0396 | E | HOMOSERINE DEHYDROGENASE. |
| | ID0397 | E | ORF starting with ATG of length 492 |
| | ID0398 | E | AMINO ACID CARRIER PROTEIN (SODIUM/ALANINE SYMPORTER). |
| | ID0399 | E | 3-HYDROXY-3-METHYLGLUTARATE-COA LYASE. |
| 40 | ID0400 | E | XAA-PRO DIPEPTIDASE. |
| | ID0401 | E | AMIDOTRANSFERASE HISH (EC 2.4.2.-). |
| | ID0402 | E | PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTID |
| | ID0403 | E | SHIKIMATE KINASE. |
| 45 | ID0404 | E | ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 3 (EC 6.3.5.4) |
| | ID0405 | E | HYDANTOINASE. |
| | ID0406 | E | HYPOTHETICAL 39.5 KDA PROTEIN. |
| | ID0407 | E | ORF starting with ATG of length 465 |
| 50 | ID0408 | E | CYSTEINE SYNTHASE. |
| | ID0409 | E | PEPTIDASE, M20/M25/M40 FAMILY. |
| | ID0410 | E | ILVA. |
| | ID0411 | E | HYPOTHETICAL 33.1 KDA PROTEIN IN MTLD-SIPU INTERGENIC REGION |
| 55 | ID0412 | E | GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUT |
| | ID0413 | E | CYCLASE. |
| | ID0414 | E | HISTIDINE BIOSYNTHESIS BIFUNCTIONAL PROTEIN HISIE [INCLUDES: |
| 60 | ID0415 | E | SA0010 PROTEIN. |
| | ID0416 | E | DIAMINOPIMELATE DECARBOXYLASE. |
| | ID0417 | E | BH3875 PROTEIN. |
| | ID0418 | E | PROBABLE PEPTIDASE YUXL (EC 3.4.21.-). |
| | ID0419 | E | ASPARTATE AMMONIA-LYASE (EC 4.3.1.1) (ASPARTASE). |
| 65 | ID0420 | E | PROBABLE AMINO-ACID ABC TRANSPORTER ATP-BINDING PROTEIN Y4TH |

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| | ID0421 (ACOAT). | E | ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11) |
| | ID0422 | E | ORNITHINE AMINOTRANSFERASE. |
| | ID0423 | E | BH3875 PROTEIN. |
| 5 | ID0424 | E | DIAMINOPIMELATE EPIMERASE. |
| | ID0425 | E | MEMBRANE PERMEASE OPUCD. |
| | ID0426 | E | AMINOTRANSFERASE REQUIRED FOR NAD BIOSYNTHESIS (NIFS |
| | PROTEIN | | |
| | ID0427 | E | GLYCINE DEHYDROGENASE SUBUNIT 2. |
| 10 | ID0428 | E | GLYCINE DEHYDROGENASE SUBUNIT 1. |
| | ID0429 | E | ORNITHINE AMINOTRANSFERASE (EC 2.6.1.13) (ORNITHINE-- |
| | OXO-ACI | | |
| | ID0430 | E | 3-DEHYDROQUINATE SYNTHASE. |
| | ID0431 | E | HISTIDASE (HISTIDINE AMMONIA-LYASE) (EC 4.3.1.3). |
| 15 | ID0432 | E | 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTTRANSFERASE. |
| | ID0433 | E | BH0606 PROTEIN. |
| | ID0434 | E | SHIKIMATE KINASE. |
| | ID0435 | E | ORF starting with ATG of length 327 |
| | ID0436 | EF | CARBAMOYL-PHOSPHATE SYNTHETASE (CATALYTIC SUBUNIT). |
| 20 | ID0437 | EF | CARBAMOYL-PHOSPHATE SYNTHETASE (CATALYTIC SUBUNIT). |
| | ID0438 | EF | CARBAMOYL-PHOSPHATE SYNTHETASE, PYRIMIDINE-SPECIFIC, |
| | SMALL CHA | | |
| | ID0439 | EF | CARBAMOYL-PHOSPHATE SYNTHETASE (CATALYTIC SUBUNIT). |
| | ID0440 | EF | ARGININE SPECIFIC CARBAMOYL-PHOSPHATE SYNTHASE |
| 25 | SUBUNIT A (EC | | |
| | ID0441 | EF | CARBAMOYL-PHOSPHATE SYNTHETASE (CATALYTIC SUBUNIT). |
| | ID0442 | EF | CARBAMOYL-PHOSPHATE SYNTHETASE (CATALYTIC SUBUNIT). |
| | ID0443 | EF | ORF starting with ATG of length 462 |
| | ID0444 | EF | CARBAMOYL-PHOSPHATE SYNTHASE LARGE SUBUNIT. |
| 30 | ID0445 | EF | ARGININE SPECIFIC CARBAMOYL-PHOSPHATE SYNTHASE |
| | SUBUNIT B (EC | | |
| | ID0446 | EF | H. pylori cytoplasmic protein 04ge10816orf2. |
| | ID0447 | EF | ARGININE SPECIFIC CARBAMOYL-PHOSPHATE SYNTHASE |
| 35 | SUBUNIT B (EC | | |
| | ID0448 | EG | HYPOTHETICAL 69.4 KDA PROTEIN IN PERR-ARGF INTERGENIC |
| | REGION | | |
| | ID0449 | EG | HYPOTHETICAL 69.4 KDA PROTEIN IN PERR-ARGF INTERGENIC |
| | REGION | | |
| | ID0450 | EH | KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86). |
| 40 | ID0451 | EH | ACETOLACTATE SYNTHASE LARGE SUBUNIT. |
| | ID0452 | EH | KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86). |
| | ID0453 | EH | ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) |
| | (AHAS) (ACE | | |
| | ID0454 | EH | ANTHRANILATE SYNTHASE. |
| 45 | ID0455 | EH | MYO-INOSITOL CATABOLISM. |
| | ID0456 | EH | ANTHRANILATE SYNTHASE BETA SUBUNIT. |
| | ID0457 | EH | PARA-AMINOBENZOATE/ANTHRANILATE SYNTHASE GLUTAMINE |
| | AMIDOTRAN | | |
| | ID0458 | EH | 4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.). |
| 50 | ID0459 | EH | PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.). |
| | ID0460 | EH | ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27). |
| | ID0461 | EH | ORF starting with ATG of length 1008 |
| | ID0462 | EH | MYO-INOSITOL CATABOLISM. |
| | ID0463 | EH | PARA-AMINOBENZOATE/ANTHRANILATE SYNTHASE GLUTAMINE |
| 55 | AMIDOTRAN | | |
| | ID0464 | EH | 4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.----) (ADC |
| | LYASE) (AD | | |
| | ID0465 | EH | ORF starting with ATG of length 840 |
| 60 | ID0466 | EH | ORF starting with TTG or GTG of length 546 |
| | ID0467 | EHR | NA+/MYO-INOSITOL COTRANSPORTER. |
| | ID0468 | EHR | HYPOTHETICAL 55.0 KDA PROTEIN IN EPR-GALK INTERGENIC |
| | REGION. | | |
| | ID0469 | EHR | HYPOTHETICAL PROTEIN HI1728. |
| | ID0470 | EHR | OSMOREGULATED PROLINE TRANSPORTER (SODIUM/PROLINE |
| 65 | SYMPORTER) | | |
| | ID0471 | EHR | NA+/MYO-INOSITOL COTRANSPORTER. |

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| | ID0472 | EHR | ORF starting with ATG of length 1269 |
| | ID0473 | EHR | BH1820 PROTEIN. |
| | ID0474 | EJ | L-ASPARAGINASE (EC 3.5.1.1) (L-ASPARAGINE AMIDOHYDROLASE) |
| 5 | ID0475 | EM | PROBABLE 5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41) |
| | ID0476 | EM | PROBABLE 5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41) |
| 10 | ID0477 | EM | HYPOTHETICAL 33.3 KDA PROTEIN IN PERR-ARGF INTERGENIC REGION |
| | ID0478 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| | ID0479 | EP | ORF starting with ATG of length 408 |
| | ID0480 | EP | DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPB. |
| 15 | ID0481 | EP | BH1159 PROTEIN. |
| | ID0482 | EP | DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC. |
| | ID0483 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| 20 | ID0484 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| | ID0485 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0486 | EP | 420AA LONG HYPOTHETICAL OLIGOPEPTIDE TRANSPORT ATP-BINDING P |
| | ID0487 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| 25 | ID0488 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| | ID0489 | EP | OPPB PROTEIN. |
| | ID0490 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 30 | ID0491 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| | ID0492 | EP | OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN APPF. |
| | ID0493 | EP | B. subtilis oppC membrane protein. |
| | ID0494 | EP | ORF starting with ATG of length 768 |
| 35 | ID0495 | EP | OLIGOPEPTIDE ABC TRANSPORTER, PERMEASE PROTEIN. |
| | ID0496 | EP | OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR. |
| | ID0497 | EP | OLIGOPEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN. |
| | ID0498 | EP | DIPEPTIDE-BINDING PROTEIN DPPE PRECURSOR. |
| | ID0499 | EP | OLIGOPEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN HOMOLOG. |
| 40 | ID0500 | EP | PROBABLE OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN APPF (FR |
| | ID0501 | EP | OLIGOPEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN. |
| | ID0502 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| 45 | ID0503 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0504 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0505 | EP | DIPEPTIDE TRANSPORT ATP-BINDING PROTEIN DPPD. |
| | ID0506 | EP | Enterococcus faecalis antigenic polypeptide fragment EF045. |
| | ID0507 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| 50 | ID0508 | EP | ORF starting with ATG of length 711 |
| | ID0509 | EP | DIPEPTIDE ABC TRANSPORTER (DIPEPTIDE-BINDING PROTEIN). |
| | ID0510 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| | ID0511 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| 55 | ID0512 | EP | DPPD PROTEIN. |
| | ID0513 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| | ID0514 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| 60 | ID0515 | EP | DIPEPTIDE ABC TRANSPORTER (PERMEASE). |
| | ID0516 | EP | DPPB PROTEIN. |
| | ID0517 | EP | DIPEPTIDE TRANSPORTER PROTEIN DPPA (FRAGMENT). |
| | ID0518 | EP | DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPB. |
| | ID0519 | EP | ORF starting with ATG of length 1161 |
| 65 | ID0520 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |

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| | ID0521 | EP | OLIGOPEPTIDE TRANSPORT SYSTEM INTEGRAL MEMBRANE PROTEIN. |
| | ID0522 | EP | DIPEPTIDE ABC TRANSPORTER (PERMEASE). |
| | ID0523 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| 5 | ID0524 | EP | OLIGOPEPTIDE ABC TRANSPORTER (OLIGOPEPTIDE-BINDING PROTEIN). |
| | ID0525 | EP | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| | ID0526 | EP | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0527 | EP | OLIGO/DIPEPTIDE TRANSPORT, ATP BINDING PROTEIN. |
| 10 | CARBOXY-END | | |
| | ID0528 | EP | OPPF PROTEIN. |
| | ID0529 | EP | SA0851 PROTEIN. |
| | ID0530 | EP | OLIGOPEPTIDE ABC TRANSPORTER, ATP-BINDING PROTEIN. |
| | ID0531 | EP | ORF starting with ATG of length 708 |
| 15 | ID0532 | EPGR | <i>Corynebacterium glutamicum</i> MCT protein SEQ ID NO:522. |
| | ID0533 | ER | GLUTAMATE SYNTHASE SMALL CHAIN. |
| | ID0534 | ER | ZINC-CONTAINING ALCOHOL DEHYDROGENASE. |
| | ID0535 | ER | GLUTAMATE SYNTHASE, BETA SUBUNIT. |
| | ID0536 | ER | DEHYDROGENASE. |
| 20 | ID0537 | ER | <i>Arabidopsis thaliana</i> protein fragment SEQ ID NO: 1993. |
| | ID0538 | ER | SORBITOL DEHYDROGENASE (EC 1.1.1.14). |
| | ID0539 | ER | SORBITOL DEHYDROGENASE (EC 1.1.1.14). |
| | ID0540 | ER | SORBITOL DEHYDROGENASE (EC 1.1.1.14). |
| 25 | ID0541 | ER | YTP. |
| | ID0542 | ER | GLUTAMATE SYNTHASE (SMALL SUBUNIT). |
| | ID0543 | ER | GLUTAMATE SYNTHASE (SMALL SUBUNIT). |
| | ID0544 | ER | FISSION YEAST (FRAGMENT). |
| | ID0545 | FE | PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE (EC 2.7.6.1). |
| 30 | ID0546 | FE | PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE (EC 2.7.6.1). |
| | ID0547 | FE | PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE (EC 2.7.6.1). |
| | ID0548 | F | PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE. |
| | ID0549 | F | ORF starting with ATG of length 531 |
| | ID0550 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE SYNTHETASE. |
| 35 | ID0551 | F | PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE. |
| | ID0552 | F | GUANYLATE KINASE (EC 2.7.4.8). |
| | ID0553 | F | CYTOSINE PERMEASE. |
| | ID0554 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDE SYNTHETASE I. |
| | ID0555 | F | DIHYDROOROTASE. |
| 40 | ID0556 | F | URACIL TRANSPORTER (PERMEASE). |
| | ID0557 | F | PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYLTRANSFERASE/IM |
| | ID0558 | F | THIAMIN BIOSYNTHESIS. |
| | ID0559 | F | TGLUTAMINE AMIDOTRANSFERASE |
| 45 | ID0560 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE SYNTHETASE. |
| | ID0561 | F | PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE. |
| | ID0562 | F | INOSINE-URIDINE NUCLEOSIDE HYDROLASE. |
| | ID0563 | F | DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE. |
| | ID0564 | F | MTA/SAH NUCLEOSIDASE (P46). |
| 50 | ID0565 | F | ASPARTATE CARBAMOYLTRANSFERASE. |
| | ID0566 | F | DIHYDROOROTASE (EC 3.5.2.3) (DHOASE). |
| | ID0567 | F | ADENYLOSUCCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL) |
| | ID0568 | F | METHYLPHOSPHOTRIESTER-DNA ALKYLTRANSFERASE. |
| 55 | ID0569 | F | THYMIDYLATE KINASE (EC 2.7.4.9). |
| | ID0570 | F | URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) (UMP PYROPHOSP) |
| | ID0571 | F | PUR OPERON REPRESSOR. |
| | ID0572 | F | CYTOSINE PERMEASE. |
| 60 | ID0573 | F | TRANSCRIPTIONAL REPRESSOR OF THE PURINE OPERON. |
| | ID0574 | F | THYMIDYLATE SYNTHASE B (EC 2.1.1.45). |
| | ID0575 | F | ORF starting with ATG of length 528 |
| | ID0576 | F | PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYLTRANSFERASE/IM |
| 65 | ID0577 | F | FORMYLtetrahydrofolate deformylase. |
| | ID0578 | F | ORF starting with ATG of length 1554 |

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| | ID0579 | F | THYMIDYLATE SYNTHASE B (EC 2.1.1.45). |
| | ID0580 | F | BH3453 PROTEIN. |
| | ID0581 | F | OROTIDINE 5'-PHOSPHATE DECARBOXYLASE. |
| | ID0582 | F | OROTATE PHOSPHORIBOSYLTRANSFERASE. |
| 5 | ID0583 | F | DIHYDROORotate DEHYDROGENASE, CATALYTIC SUBUNIT (EC 1.3.3.1). |
| | ID0584 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHETASE I. |
| | ID0585 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHETASE II. |
| 10 | ID0586 | F | D-HYDANTOINASE (EC 3.5.2.2) (DIHYDROPRIMIDINASE) (DHPASE). |
| | ID0587 | F | PROBABLE OXIDOREDUCTASE. |
| | ID0588 | F | XANTHINE PHOSPHORIBOSYLTRANSFERASE. |
| | ID0589 | F | PUTATIVE INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE. |
| 15 | ID0590 | F | NUCLEOSIDE TRANSPORTER. |
| | ID0591 | F | BH1014 PROTEIN. |
| | ID0592 | F | ADENINE DEAMINASE (EC 3.5.4.2) (ADENASE) (ADENINE AMINASE). |
| 20 | ID0593 | F | ADENINE DEAMINASE. |
| | ID0594 | F | PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.2). |
| | ID0595 | F | ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE). |
| | ID0596 | F | ADENINE DEAMINASE. |
| 25 | ID0597 | F | LATE COMPETENCE OPERON REQUIRED FOR DNA BINDING AND UPTAKE. |
| | ID0598 | F | THYMIDINE KINASE (EC 2.7.1.21). |
| | ID0599 | F | CYTOSINE PERMEASE/TRANSPORT. |
| | ID0600 | F | S. pneumoniae adenylosuccinate lyase. |
| 30 | ID0601 | F | ADENYLOSUCCINATE SYNTHETASE. |
| | ID0602 | F | GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2) (GLUTAMINE). |
| | ID0603 | F | ADENINE PHOSPHORIBOSYLTRANSFERASE. |
| | ID0604 | F | NUCLEOTIDASE PRECURSOR. |
| 35 | ID0605 | F | ORF starting with ATG of length 247 |
| | ID0606 | F | GMP SYNTHETASE. |
| | ID0607 | F | CYTIDYLATE KINASE (EC 2.7.4.14) (CK) (CYTIDINE). |
| | ID0608 | F | RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE BETA CHAIN (EC 1.17.4.1). |
| 40 | ID0609 | F | RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4). |
| | ID0610 | F | BH1015 PROTEIN. |
| | ID0611 | F | BH1015 PROTEIN. |
| | ID0612 | F | MTA/SAH NUCLEOSIDASE (P46). |
| 45 | ID0613 | F | TRANSCRIPTIONAL ATTENUATION OF THE PYRIMIDINE OPERON/URACILP. |
| | ID0614 | F | URACIL TRANSPORTER (PERMEASE). |
| | ID0615 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE SUCCINOCARBOXAMIDE SYNTHETASE. |
| 50 | ID0616 | F | ORF starting with ATG of length 1377 |
| | ID0617 | F | ADENYLOSUCCINATE LYASE. |
| | ID0618 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE SUCCINOCARBOXAMIDE SYNTHETASE. |
| | ID0619 | F | BH0627 PROTEIN. |
| 55 | ID0620 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE I (EC 6.3.5.3) (F). |
| | ID0621 | F | FGAM SYNTHETASE (FRAGMENT). |
| | ID0622 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHETASE I. |
| | ID0623 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHETASE I. |
| 60 | ID0624 | F | URACIL TRANSPORTER (PERMEASE). |
| | ID0625 | F | PHOSPHORIBOSYLAMINOIMIDAZOLE SUCCINOCARBOXAMIDE SYNTHETASE. |
| | ID0626 | F | BH0627 PROTEIN. |
| | ID0627 | F | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHETASE II. |
| 65 | ID0628 | F | BH1014 PROTEIN. |
| | ID0629 | F | DNA TOPOLOGY MODULATION PROTEIN FLAR-RELATED PROTEIN. |

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| | ID0630 | F | HYPOTHETICAL 43.5 KDA PROTEIN. |
| | ID0631 | F | ADENINE PHOSPHORIBOSYLTRANSFERASE. |
| | ID0632 | FGR | HIT-LIKE PROTEIN INVOLVED IN CELL-CYCLE REGULATION. |
| 5 | ID0633 | FGR | ORF starting with ATG of length 333 |
| | ID0634 | FGR | CELL-CYCLE REGULATION HISTIDINE TRIAD (HIT FAMILY). |
| | ID0635 | FJ | HYPOTHETICAL 17.8 KDA PROTEIN IN SERS-DNAH INTERGENIC |
| | REGION | | |
| | ID0636 | FJ | YKOA. |
| 10 | ID0637 | FR | BH1692 PROTEIN. |
| | ID0638 | FR | HYPOTHETICAL PROTEIN MTH1505. |
| | ID0639 | FR | <i>E. coli</i> cytosine-deaminase. |
| | ID0640 | GC | HYPOTHETICAL GLYCOSYL TRANSFERASE. |
| | ID0641 | GE | GLUCONATE PERMEASE. |
| | ID0642 | GE | BH3897 PROTEIN. |
| 15 | ID0643 | GE | LOW-AFFINITY GLUCONATE TRANSPORTER (GLUCONATE |
| | PERMEASE) (GNT | | |
| | ID0644 | GE | BH3897 PROTEIN. |
| | ID0645 | GE | GLUCONATE PERMEASE. |
| 20 | ID0646 | GE | PUTATIVE GLUCONATE PERMEASE (FRAGMENT). |
| | ID0647 | GE | GNTP (GLUCONATE PERMEASE). |
| | ID0648 | GE | PUTATIVE GLUCONATE PERMEASE (FRAGMENT). |
| | ID0649 | GE | GLUCONATE PERMEASE. |
| | ID0650 | GE | GNTP (GLUCONATE PERMEASE). |
| | ID0651 | GE | BH3897 PROTEIN. |
| 25 | ID0652 | GEPR | BH1161 PROTEIN. |
| | ID0653 | GEPR | MULTIDRUG RESISTANCE EFFLUX PUMP. |
| | ID0654 | GEPR | BH1161 PROTEIN. |
| | ID0655 | GEPR | PUTATIVE SUGAR EFFLUX TRANSPORTER DR1322. |
| 30 | ID0656 | GEPR | ORF starting with ATG of length 432 |
| | ID0657 | GEPR | ORF starting with ATG of length 534 |
| | ID0658 | GEPR | ORF starting with ATG of length 1077 |
| | ID0659 | GEPR | ORF starting with ATG of length 735 |
| | ID0660 | GEPR | ORF starting with ATG of length 1092 |
| 35 | ID0661 | GEPR | MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX |
| | TRANSPORTER | | |
| | ID0662 | GEPR | MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX |
| | TRANSPORTER | | |
| | ID0663 | GEPR | ORF starting with ATG of length 885 |
| | ID0664 | GEPR | HYPOTHETICAL 44.9 KDA PROTEIN. |
| 40 | ID0665 | GEPR | TRANSPORTER. |
| | ID0666 | GEPR | HOMOLOGUE OF MULTIDRUG RESISTANCE PROTEIN B, EMRB, OF |
| | E. COL | | |
| | ID0667 | GER | BH0725 PROTEIN. |
| | ID0668 | GER | ORF starting with ATG of length 522 |
| 45 | ID0669 | GER | HYPOTHETICAL 33.6 KDA PROTEIN IN CSPC-NAP INTERGENIC |
| | REGION. | | |
| | ID0670 | GER | BH1931 PROTEIN. |
| | ID0671 | G | LACTOSE TRANSPORT SYSTEM PERMEASE PROTEIN LACG. |
| | ID0672 | G | PROBABLE ABC-TRANSPORT PROTEIN, INNER MEMBRANE |
| 50 | COMPONENT. | | |
| | ID0673 | G | PUTATIVE TRANSPORT SYSTEM INNER MEMBRANE PROTEIN. |
| | ID0674 | G | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID0675 | G | PUTATIVE PTS ENZYME III. |
| | ID0676 | G | PHOSPHOENOLPYRUVATE MUTASE. |
| 55 | ID0677 | G | GALACTOKINASE. |
| | ID0678 | G | L-ARABINOSE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0679 | G | L-ARABINOSE MEMBRANE PERMEASE. |
| | ID0680 | G | PUTATIVE TRANSKETOLASE N-TERMINAL SECTION (EC |
| | 2.2.1.1) (TK). | | |
| 60 | ID0681 | G | HYPOTHETICAL 37.6 KDA PROTEIN. |
| | ID0682 | G | <i>Arabidopsis thaliana</i> protein fragment SEQ ID NO: |
| | 43508. | | |
| | ID0683 | G | Lung cancer associated polypeptide sequence SEQ ID |
| | 769. | | |
| 65 | ID0684 | G | Paenibacillus pabuli 2,6-beta-D-fructan hydrolase. |
| | ID0685 | G | <i>Streptococcus pneumoniae</i> photomutase yhxB. |

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| | ID0686 | G | SUGAR ABC TRANSPORTER (PERMEASE). |
| | ID0687 | G | BETA-GLUCOSIDASE (EC 3.2.1.21). |
| | ID0688 | G | XYLOSIDASE/ARABINOSIDASE [INCLUDES: BETA-XYLOSIDASE (EC 3.2.1.22)]. |
| 5 | ID0689 | G | ALPHA-GLUCURONIDASE. |
| | ID0690 | G | RHAMNULOKINASE. |
| | ID0691 | G | SA0233 PROTEIN. |
| | ID0692 | G | SUGAR HYDROLASE. |
| 10 | ID0693 | G | ORF starting with ATG of length 348 |
| | ID0694 | G | ALGM1. |
| | ID0695 | G | TRANSMEMBRANE LIPOPROTEIN. |
| | ID0696 | G | S. pneumoniae derived protein #253. |
| | ID0697 | G | PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (EC 2.7.3.9). |
| 15 | ID0698 | G | ALTRONATE HYDROLASE. |
| | ID0699 | G | GLUCONOKINASE (EC 2.7.1.12) (GLUCONATE KINASE). |
| | ID0700 | G | ALPHA-GLUCOSIDASE. |
| | ID0701 | G | PHOSPHO-CELLOBIASE (EC 3.2.1.1). |
| 20 | ID0702 | G | ORF starting with ATG of length 906 |
| | ID0703 | G | YBCL PROTEIN. |
| | ID0704 | G | ABC TRANSPORTER SUGAR PERMEASE. |
| | ID0705 | G | ABC TRANSPORTER SUGAR PERMEASE. |
| | ID0706 | G | BETA-GALACTOSIDASE. |
| | ID0707 | G | PUTATIVE N-ACETYLmannosamine-6-P EPIMERASE. |
| 25 | ID0708 | G | GLUCONATE-6-PHOSPHATE DEHYDROGENASE, DECARBOXYLATING. |
| | ID0709 | G | BH1117 PROTEIN. |
| | ID0710 | G | PUTATIVE GLUTAMYL-AMINOPEPTIDASE (FRAGMENT). |
| | ID0711 | G | ENDO-1,4-BETA-GLUCANASE. |
| 30 | ID0712 | G | Non-maltogenic exoamylase amino acid sequence. |
| | ID0713 | G | Non-maltogenic exoamylase amino acid sequence. |
| | ID0714 | G | ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PH 4.2.1.11). |
| | ID0715 | G | ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (EC 4.2.1.11). |
| 35 | ID0716 | G | Enterococcus faecalis protein EF048. |
| | ID0717 | G | XYLQ. |
| | ID0718 | G | PROBABLE SUGAR TRANSPORT PROTEIN (PERMEASE). |
| | ID0719 | G | BH1905 PROTEIN. |
| 40 | ID0720 | G | PROBABLE FRUCTOSE-BISPHOSPHATE ALDOLASE 2 (EC 4.1.2.13). |
| | ID0721 | G | SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA. |
| | ID0722 | G | 6-PHOSPHO-BETA-GLUCOSIDASE. |
| 45 | ID0723 | G | SUGAR TRANSPORT SYSTEM (PERMEASE) (BINDING PROTEIN DEPENDENT). |
| | ID0724 | G | HYPOTHETICAL 38.4 KDA PROTEIN IN DPPE-HMP INTERGENIC REGION. |
| | ID0725 | G | PROBABLE ABC-TRANSPORT PROTEIN, INNER MEMBRANE COMPONENT. |
| 50 | ID0726 | G | BETA-GLUCOSIDASE. |
| | ID0727 | G | HYPOTHETICAL 48.4 KDA PROTEIN. |
| | ID0728 | G | MALTOSE TRANSPORTOR ATP-BINDING PROTEIN. |
| | ID0729 | G | SUGAR ABC TRANSPORTER (PERMEASE). |
| | ID0730 | G | PUTATIVE CARBOXYVINYL-CARBOXYPHOSPHONATE |
| 55 | PHOSPHORYLMUTASE (EC | | PTS SYSTEM, FRUCTOSE-SPECIFIC IIABC COMPONENT (FRUA-1). |
| | ID0731 | G | PTS SYSTEM, FRUCTOSE-SPECIFIC IIABC COMPONENT (FRUA-1). |
| | ID0732 | G | PTS SYSTEM, MANNITOL-1-PHOSPHATE DEHYDROGENASE (ENZYME III). |
| 60 | ID0733 | G | SUCROSE-6-P HYDROLASE. |
| | ID0734 | G | PUTATIVE SUCROSE-SPECIFIC PTS PERMEASE, ENZYME II. |
| | ID0735 | G | DEOXYPHOSPHOGLUCONATE ALDOLASE. |
| | ID0736 | G | TRANSMEMBRANE LIPOPROTEIN. |
| | ID0737 | G | SUGAR ABC TRANSPORTER (PERMEASE). |
| 65 | ID0738 | G | ENDO-1,4-BETA-KYLANASE. |

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| | ID0739 | G | SUGAR TRANSPORT SYSTEM (PERMEASE) (BINDING PROTEIN |
| | DEPENDENT | | |
| | ID0740 | G | S. pneumoniae derived protein #302. |
| | ID0741 | G | FRUCTOSE BISPHOSPHATE ALDOLASE. |
| 5 | ID0742 | G | BH1074 PROTEIN. |
| | ID0743 | G | SA0233 PROTEIN. |
| | ID0744 | G | ALPHA-GALACTOSIDASE. |
| | ID0745 | G | URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE |
| | ISOMERASE) (URO | | |
| 10 | ID0746 | G | ORF starting with ATG of length 633 |
| | ID0747 | G | endo 1,5 alpha-L-arabinase |
| | ID0748 | G | BETA-XYLOSIDASE / ALPHA-L-ARABINOSIDASE. |
| | ID0749 | G | FBAA. |
| | ID0750 | G | ORF starting with ATG of length 558 |
| 15 | ID0751 | G | ALPHA-GALACTOSIDASE (EC 3.2.1.22) (MELIBIASE). |
| | ID0752 | G | ALPHA-GALACTOSIDASE (EC 3.2.1.22) (MELIBIASE). |
| | ID0753 | G | 6-PHOSPHO-BETA-GLUCOSIDASE. |
| | ID0754 | G | L-ARABINOSE MEMBRANE PERMEASE. |
| 20 | ID0755 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA- |
| | CEL) (CE | | |
| | ID0756 | G | Streptococcus pneumoniae type 4 protein sequence #56. |
| | ID0757 | G | ALPHA-GALACTOSIDASE (EC 3.2.1.22) (MELIBIASE). |
| | ID0758 | G | XYLOSE ISOMERASE (EC 5.3.1.5). |
| | ID0759 | G | BH1878 PROTEIN. |
| 25 | ID0760 | G | LIPOPROTEIN. |
| | ID0761 | G | TRANSMEMBRANE LIPOPROTEIN. |
| | ID0762 | G | ABC TRANSPORTER (PERMIASE). |
| | ID0763 | G | ENDO-1,4-BETA-GLUCANASE. |
| | ID0764 | G | 362AA LONG HYPOTHETICAL MALTOSE/MALTODEXTRIN |
| 30 | TRANSPORT ATP-B | | |
| | ID0765 | G | FRUCTOKINASE. |
| | ID0766 | G | BH1117 PROTEIN. |
| | ID0767 | G | LACTOSE TRANSPORT SYSTEM (PERMEASE). |
| | ID0768 | G | ORF starting with ATG of length 666 |
| 35 | ID0769 | G | GLUCOSIDASE. |
| | ID0770 | G | SUGAR TRANSPORT SYSTEM (PERMEASE) (BINDING PROTEIN |
| | DEPENDENT | | |
| | ID0771 | G | SULFATE ABC TRANSPORTER, ATP-BINDING PROTEIN. |
| | ID0772 | G | 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE |
| 40 | MUTASE. | | |
| | ID0773 | G | LIPOPROTEIN. |
| | ID0774 | G | PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC- |
| | FRU) (FR | | |
| | ID0775 | G | PHOSPHOTRANSFERASE SYSTEM (PTS) FRUCTOSE-SPECIFIC |
| 45 | ENZYME IIB | | |
| | ID0776 | G | PHOSPHOGLYCERATE KINASE (EC 2.7.2.3). |
| | ID0777 | G | TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM). |
| | ID0778 | G | ORF starting with ATG of length 774 |
| | ID0779 | G | PHOSPHOMANOMUTASE. |
| 50 | ID0780 | G | Recombinant glucose-6-phosphate dehydrogenase. |
| | ID0781 | G | MELIBIASE (ALPHA-GALACTOSIDASE) (EC 3.2.1.22). |
| | ID0782 | G | 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC |
| | 1.1.1. | | |
| | ID0783 | G | HYPOTHETICAL 24.5 KDA PROTEIN. |
| 55 | ID0784 | G | ORF starting with ATG of length 642 |
| | ID0785 | G | PUTATIVE SUGAR HYDROLASE. |
| | ID0786 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC ENZYME II, B |
| | COMPONENT (EIIA | | |
| | ID0787 | G | ORF starting with ATG of length 375 |
| 60 | ID0788 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC ENZYME II, C |
| | COMPONENT (EIIA | | |
| | ID0789 | G | HYPOTHETICAL 38.7 KDA PROTEIN. |
| | ID0790 | G | PUTATIVE SUGAR TRANSPORT SYSTEM PERMEASE PROTEIN. |
| | ID0791 | G | ORF starting with ATG of length 615 |
| 65 | ID0792 | G | HYPOTHETICAL 54.3 KDA PROTEIN. |
| | ID0793 | G | PUTATIVE SUGAR ABC TRANSPORTER (ATP-BINDING PROTEIN). |

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| | ID0794 | G | PUTATIVE CARBOXYVINYL-CARBOXYPHOSPHONATE |
| | PHOSPHORYLMUTASE (EC | | |
| | ID0795 | G | PTS SYSTEM, FRUCTOSE-SPECIFIC ENZYME II, BC |
| | COMPONENT. | | |
| 5 | ID0796 | G | 1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56) (FRUCTOSE 1- |
| | PHOSPHATE KI | | |
| | ID0797 | G | PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC |
| | COMPONENT | | |
| 10 | ID0798 | G | PUTATIVE TRANSKETOLASE C-TERMINAL SECTION (EC |
| | 2.2.1.1) (TK). | | |
| | ID0799 | G | EXO-INULINASE. |
| | ID0800 | G | SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) (SUCRASE) |
| | (INVER | | |
| 15 | ID0801 | G | SURFACE PROTEIN PLS. |
| | ID0802 | G | YBCL PROTEIN. |
| | ID0803 | G | SUCROSE-6-PHOSPHATE HYDROLASE. |
| | ID0804 | G | PYRUVATE KINASE (EC 2.7.1.40) (PK). |
| | ID0805 | G | PHOSPHOCARRIER PROTEIN HPR (CATABOLITE REPRESSION). |
| 20 | ID0806 | G | BH0789 PROTEIN. |
| | ID0807 | G | PUTATIVE SUCROSE-SPECIFIC PTS PERMEASE, ENZYME II. |
| | ID0808 | G | SCRB. |
| | ID0809 | G | L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17) (L- |
| | FUCULOSE-1-PH | | |
| 25 | ID0810 | G | FRUCTOSE-SPECIFIC PTS SYSTEM ENZYME IIIBC COMPONENT |
| | (EC 2.7.1 | | |
| | ID0811 | G | 6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11) |
| | (PHOSPHOFRUCTOKINASE) (PH | | |
| | ID0812 | G | HYPOTHETICAL 40.2 KDA PROTEIN. |
| 30 | ID0813 | G | ORF starting with ATG of length 975 |
| | ID0814 | G | PUTATIVE SUCROSE-SPECIFIC PTS PERMEASE, ENZYME II. |
| | ID0815 | G | HYPOTHETICAL PROTEIN HI1028 PRECURSOR. |
| | ID0816 | G | LACTOSE TRANSPORT SYSTEM (PERMEASE). |
| | ID0817 | G | BH1117 PROTEIN. |
| 35 | ID0818 | G | CHLORAMPHENICOL RESISTANCE PROTEIN. |
| | ID0819 | G | PROTEIN HI0146 PRECURSOR. |
| | ID0820 | G | Streptococcus pneumoniae type 4 protein sequence #18. |
| | ID0821 | G | HYPOTHETICAL 43.3 KDA PROTEIN. |
| | ID0822 | G | HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YURN. |
| 40 | ID0823 | G | ORF starting with ATG of length 454 |
| | ID0824 | G | MYO-INOSITOL CATABOLISM. |
| | ID0825 | G | B. subtilis hexulose phosphate synthase. |
| | ID0826 | G | MALTOSE/MALTODEXTRIN TRANSPORT SYSTEM (PERMEASE). |
| | ID0827 | G | SA2241 PROTEIN. |
| | ID0828 | G | YBCL PROTEIN. |
| 45 | ID0829 | G | ORF starting with ATG of length 861 |
| | ID0830 | G | SA0233 PROTEIN. |
| | ID0831 | G | ZY044582 signal trapped geneweak similarity to yeso |
| | type gen | | |
| | ID0832 | G | TRANSMEMBRANE LIPOPROTEIN. |
| 50 | ID0833 | G | ABC TRANSPORTER (PERMIASE). |
| | ID0834 | G | 2-KETO-3-DEOXY-GLUCONATE KINASE. |
| | ID0835 | G | D-MANNONATE HYDROLASE. |
| | ID0836 | G | ORF starting with ATG of length 385 |
| | ID0837 | G | ORF starting with ATG of length 680 |
| 55 | ID0838 | G | XYLOSE ISOMERASE (EC 5.3.1.5). |
| | ID0839 | G | XYLULOSE KINASE (EC 2.7.1.17) (XYLULOKINASE). |
| | ID0840 | G | SUCROSE-SPECIFIC PTS PERMEASE. |
| | ID0841 | G | XYLOSIDASE/ARABINOSIDASE [INCLUDES: BETA-XYLOSIDASE |
| | (EC 3.2. | | |
| 60 | ID0842 | G | MYO-INOSITOL CATABOLISM. |
| | ID0843 | G | SUGAR TRANSPORT SYSTEM (PERMEASE). |
| | ID0844 | G | CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1.). |
| | ID0845 | G | ARAD. |
| 65 | ID0846 | G | SUGAR ABC TRANSPORTER (PERMEASE). |
| | ID0847 | G | ORF starting with ATG of length 534 |
| | ID0848 | G | SUGAR FERMENTATION STIMULATION PROTEIN. |

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| | ID0849 | G | PHOSPHOMANNOMUTASE. |
| | ID0850 | G | PHOSPHOGLUCOSAMINE MUTASE. |
| | ID0851 | G | BH0285 PROTEIN. |
| | ID0852 | G | BH1066 PROTEIN. |
| 5 | ID0853 | G | INTEGRAL MEMBRANE PROTEIN. |
| | ID0854 | G | LIPOPROTEIN. |
| | ID0855 | G | N-ACETYLGLUCOSAMINE-SPECIFIC IIABC COMPONENT. |
| | ID0856 | G | GLUCOSIDASE. |
| | ID0857 | G | SUGAR ABC TRANSPORTER (PERMEASE). |
| 10 | ID0858 | G | PTS SYSTEM FRUCTOSE-LIKE IIB COMPONENT 1. |
| | ID0859 | G | N-ACETYLGLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10). |
| | ID0860 | G | GLUCOSAMINE-6-ISOMERASE. |
| | ID0861 | G | PROTEIN YCGS. |
| 15 | ID0862 | G | ORF starting with ATG of length 435 |
| | ID0863 | G | SUGAR TRANSPORT SYSTEM (PERMEASE). |
| | ID0864 | G | ORF starting with ATG of length 520 |
| | ID0865 | G | PTS SYSTEM, SUCROSE-SPECIFIC IIIBC COMPONENT (EIIBC-SCR) (SUC) |
| 20 | ID0866 | G | RHAMNULOKINASE. |
| | ID0867 | G | L-ARABINOSE ISOMERASE. |
| | ID0868 | G | SA1198 PROTEIN. |
| | ID0869 | G | LPLB PROTEIN. |
| | ID0870 | G | S. pneumoniae derived protein #253. |
| 25 | ID0871 | G | TRANSKETOLASE (EC 2.2.1.1). |
| | ID0872 | G | PROBABLE ABC-TRANSPORT PROTEIN, INNER MEMBRANE COMPONENT. |
| | ID0873 | G | GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9) (PHOSPH) |
| 30 | ID0874 | G | PHOSPHOGLUCOSAMINE MUTASE. |
| | ID0875 | G | BH0222 PROTEIN. |
| | ID0876 | G | PUTATIVE TRANSPORT SYSTEM INNER MEMBRANE PROTEIN. |
| | ID0877 | G | LACTOSE TRANSPORT SYSTEM (PERMEASE). |
| 35 | ID0878 | G | ORF starting with ATG of length 672 |
| | ID0879 | G | SUGAR TRANSPORT SYSTEM (PERMEASE) (BINDING PROTEIN DEPENDENT) |
| | ID0880 | G | ORF starting with ATG of length 375 |
| | ID0881 | G | SUGAR ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID0882 | G | SUGAR TRANSPORT SYSTEM (SUGAR-BINDING PROTEIN). |
| 40 | ID0883 | G | GLYCEROL-3-PHOSPHATE ABC TRANSPORTER (PERMEASE). |
| | ID0884 | G | GLYCEROL-3-PHOSPHATE ABC TRANSPORTER (PERMEASE). |
| | ID0885 | G | TEICHOIC ACID TRANSLOCATION ATP-BINDING PROTEIN TAGH. |
| | ID0886 | G | ABC-TRANSPORTER ATP-BINDING PROTEIN. |
| | ID0887 | G | ALTRONATE HYDROLASE. |
| 45 | ID0888 | G | Streptococcus pneumoniae SP0014 protein. |
| | ID0889 | G | SUGAR BINDING PROTEIN |
| | ID0890 | G | 6-PHOSPHO-BETA-GLUCOSIDASE. |
| | ID0891 | G | FRUCTOSE 1-PHOSPHATE KINASE. |
| | ID0892 | G | BETA-GLUCOSIDASE. |
| 50 | ID0893 | G | GLCA PROTEIN. |
| | ID0894 | G | HYPOTHETICAL 24.3 KDA PROTEIN. |
| | ID0895 | G | ABC TRANSPORTER SUGAR PERMEASE. |
| | ID0896 | G | ORF starting with ATG of length 369 |
| | ID0897 | G | METHYLGLYOXAL SYNTHASE (EC 4.2.99.11). |
| 55 | ID0898 | G | BH0592 PROTEIN. |
| | ID0899 | G | SUGAR TRANSPORT SYSTEM (PERMEASE). |
| | ID0900 | G | MYO-INOSITOL CATABOLISM. |
| | ID0901 | G | ORF starting with ATG of length 714 |
| | ID0902 | G | SUCROSE-6-PHOSPHATE HYDROLASE. |
| 60 | ID0903 | G | D-MANNONATE HYDROLASE. |
| | ID0904 | G | SA2244 PROTEIN. |
| | ID0905 | G | MULTIPLE SUGAR TRANSPORT SYSTEM (MULTIPLE SUGAR-BINDING PROT) |
| | ID0906 | G | ALTRONATE OXIDOREDUCTASE. |
| 65 | ID0907 | G | DIHYDROXYACETONE KINASE. |

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| | ID0908 | G | PTS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT (EIIABC-GLC) (G |
| | ID0909 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC ENZYME II, B |
| 5 | COMPONENT (EIIIA | | |
| | ID0910 | G | DECARBOXYLATING 6-PHOSPHOGLUCONATE DEHYDROGENASE (EC 1.1.1.4 |
| | ID0911 | G | ALTRONATE OXIDOREDUCTASE. |
| | ID0912 | G | HYPOTHETICAL 54.3 KDA PROTEIN. |
| 10 | ID0913 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA-CEL) (CE |
| | ID0914 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC ENZYME II, C |
| | COMPONENT. | | |
| | ID0915 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC IIB COMPONENT (EIIIB-CEL) (CE |
| 15 | ID0916 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC ENZYME II, C |
| | COMPONENT. | | |
| | ID0917 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA-CEL) (CE |
| 20 | ID0918 | G | HYPOTHETICAL 54.3 KDA PROTEIN. |
| | ID0919 | G | ALTRONATE HYDROLASE. |
| | ID0920 | G | MALTOSE TRANSPORTOR ATP-BINDING PROTEIN. |
| | ID0921 | G | 6-PHOSPHO-BETA-GLUCOSIDASE. |
| | ID0922 | G | MALTOGENIC AMYLASE. |
| 25 | ID0923 | G | BH1066 PROTEIN. |
| | ID0924 | G | INTEGRAL MEMBRANE PROTEIN. |
| | ID0925 | G | ORF starting with ATG of length 529 |
| | ID0926 | G | ALPHA,ALPHA-PHOSPHOTREHALASE (EC 3.2.1.93). |
| | ID0927 | G | PHOSPHOCARRIER PROTEIN HPR (CATABOLITE REPRESSION). |
| 30 | ID0928 | G | KBAY. |
| | ID0929 | G | LACTOSE TRANSPORT SYSTEM (PERMEASE). |
| | ID0930 | G | Streptococcus pneumoniae type 4 protein sequence #55. |
| | ID0931 | G | 6-PHOSPHO-BETA-GLUCOSIDASE A, CRYPTIC. |
| | ID0932 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA-CEL) (CE |
| 35 | ID0933 | G | ORF starting with ATG of length 552 |
| | ID0934 | G | 6-PHOSPHOGLUCONATE DEHYDROGENASE (EC 1.1.1.44). |
| | ID0935 | G | Recombinant glucose-6-phosphate dehydrogenase. |
| | ID0936 | G | Recombinant glucose-6-phosphate dehydrogenase. |
| 40 | ID0937 | G | ORF starting with ATG of length 924 |
| | ID0938 | G | HYPOTHETICAL PROTEIN. |
| | ID0939 | G | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID0940 | G | BETA-GLUCOSIDE SPECIFIC TRANSPORT PROTEIN. |
| | ID0941 | G | PROBABLE HEXULOSE-6-PHOSPHATE SYNTHASE (EC 4.1.2.-) (HUMPS) |
| 45 | ID0942 | G | 2-KETO-3-DEOXYGLUCONATE KINASE (EC 2.7.1.45). |
| | ID0943 | G | HYPOTHETICAL 38.7 KDA PROTEIN. |
| | ID0944 | G | YTCQ. |
| | ID0945 | G | PUTATIVE SUGAR HYDROLASE. |
| | ID0946 | G | PTS SYSTEM, CELLOBIOSE-SPECIFIC ENZYME II, C |
| 50 | COMPONENT (EIIIA | | |
| | ID0947 | G | TRANSKETOLASE, C-TERMINAL SECTION (TKT-2) (EC 2.2.1.1). |
| | ID0948 | G | FRUCTOSE-SPECIFIC PTS SYSTEM ENZYME IIBC COMPONENT (EC 2.7.1 |
| 55 | ID0949 | G | ORF starting with ATG of length 2064 |
| | ID0950 | G | MYO-INOSITOL CATABOLISM. |
| | ID0951 | G | TRIOSEPHOSPHATE ISOMERASE. |
| | ID0952 | G | P-NITROPHENYL PHOSPHATASE. |
| | ID0953 | G | CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1.). |
| 60 | ID0954 | G | ORF starting with ATG of length 612 |
| | ID0955 | G | ORF starting with ATG of length 222 |
| | ID0956 | G | ORF starting with ATG of length 552 |
| | ID0957 | GR | YOAN. |
| | ID0958 | GR | YOAN. |
| | ID0959 | GR | YOAN. |
| 65 | ID0960 | GR | ORF starting with ATG of length 330 |

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| | ID0961 ENZYME IIB | GT | PHOSPHOTRANSFERASE SYSTEM (PTS) FRUCTOSE-SPECIFIC |
| | ID0962 MTL). | GT | PTS SYSTEM MANNITOL-SPECIFIC COMPONENT IIA (EIIA- |
| 5 | ID0963 COMPONENT. | GT | MANNITOL ENZYME IIA. |
| | ID0964 COMPONENT. | GT | PTS SYSTEM, FRUCTOSE-SPECIFIC ENZYME II, BC |
| | ID0965 | GT | MANNITOL ENZYME IIA. |
| 10 | ID0966 COMPONENT. | GT | PTS SYSTEM, FRUCTOSE-SPECIFIC ENZYME II, BC |
| | ID0967 | GT | HYPOTHETICAL 16.1 KDA PROTEIN. |
| | ID0968 | GT | ORF starting with ATG of length 410 |
| | ID0969 SUBUNIT). | HC | DIHYDROORotate DEHYDROGENASE (ELECTRON TRANSFER |
| 15 | ID0970 SUBUNIT). | HC | DIHYDROORotate DEHYDROGENASE (ELECTRON TRANSFER |
| | ID0971 | HE | PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52). |
| | ID0972 | HE | PHOSPHOSERINE AMINOTRANSFERASE. |
| | ID0973 | H | THID. |
| 20 | ID0974 | H | FOLYL-POLYGLUTAMATE SYNTHETASE (EC 6.3.2.17). |
| | ID0975 | H | ORF starting with ATG of length 483 |
| | ID0976 | H | ABC TRANSPORT SYSTEM PERMEASE PROTEIN. |
| | ID0977 | H | GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE. |
| | ID0978 | H | FLAVOPROTEIN. |
| 25 | ID0979 | H | MOLYBDOPTERIN BIOSYNTHESIS PROTEIN. |
| | ID0980 | H | ORF starting with ATG of length 552 |
| | ID0981 | H | MOLYBDOPTERIN CONVERTING FACTOR (SUBUNIT 2). |
| | ID0982 | H | ORF starting with ATG of length 823 |
| 30 | ID0983 | H | BH1752 PROTEIN. |
| | ID0984 | H | RIBOFLAVIN KINASE / FAD SYNTHASE. |
| | ID0985 CYCLOHYD | H | RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBA [INCLUDES: GTP |
| | ID0986 | H | DGOA PROTEIN [INCLUDES: 2-DEHYDRO-3- |
| | DEOXYPHOSPHOGALACTONATE | | |
| 35 | ID0987 (SPORE GE | H | 2-HEPTAPRENYL-1,4-NAPHTHOQUINONE METHYLTRANSFERASE |
| | ID0988 | H | YQHM PROTEIN. |
| | ID0989 | H | SA1729 PROTEIN. |
| | ID0990 DIPHOSPHATE | H | GERANYLTRANSTRANSFERASE (EC 2.5.1.10) (FARNESYL- |
| | ID0991 | H | GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE. |
| | ID0992 | H | PROBABLE AROMATIC ACID DECARBOXYLASE (EC 4.1.1.-). |
| | ID0993 | H | NH3-DEPENDENT NAD SYNTHETASE (EC 6.3.1.5). |
| | ID0994 | H | BH1752 PROTEIN. |
| 45 | ID0995 | H | TRANSCRIPTIONAL REPRESSOR OF THE BIOTIN OPERON. |
| | ID0996 2.5.1.30) | H | HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC |
| | ID0997 | H | SPORE GERMINATION PROTEIN C3 (FRAGMENT). |
| | ID0998 | H | 4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE. |
| 50 | ID0999 | H | PUTATIVE OCTAPRENYLTRANSFERASE. |
| | ID1000 | H | PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG. |
| | ID1001 | H | DIHYDROFOLATE REDUCTASE (EC 1.5.1.3). |
| | ID1002 5.4.3.8) (GSA | H | GLUTAMATE-1-SEMALDEHYDE 2,1-AMINOMUTASE 2 (EC |
| 55 | ID1003 | H | BH1752 PROTEIN. |
| | ID1004 | H | BH1752 PROTEIN. |
| | ID1005 DIPHOSPHATE | H | GERANYLTRANSTRANSFERASE (EC 2.5.1.10) (FARNESYL- |
| | ID1006 | H | CYSG. |
| 60 | ID1007 | H | DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24). |
| | ID1008 | H | PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8). |
| | ID1009 MoeB. | H | S. carnosus nitrate reductase molybdenum cofactor |
| | ID1010 | H | MOLYBDOPTERIN BIOSYNTHESIS. |
| 65 | ID1011 | H | ABC TRANSPORT SYSTEM PERMEASE PROTEIN. |
| | ID1012 | H | ASPARTATE 1-DECARBOXYLASE. |

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| | ID1013 | H | PANTOATE BETA-ALANINE LIGASE. |
| | ID1014 | H | Cis-epoxysuccinate hydrolase alpha subunit amino acid sequen |
| | ID1015 | H | TRANSCRIPTIONAL REGULATOR. |
| 5 | ID1016 | H | DIHYDROFOLATE REDUCTASE (EC 1.5.1.3). |
| | ID1017 | H | UNKNOWN (PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN). |
| | ID1018 | H | HYPOTHETICAL PROTEIN VC0880. |
| | ID1019 | H | PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN PDXA. |
| | ID1020 | H | Cis-epoxysuccinate hydrolase alpha subunit amino acid sequen |
| 10 | ID1021 | H | UROPORPHYRINOGEN III DECARBOXYLASE. |
| | ID1022 | H | BH3930 PROTEIN. |
| | ID1023 | H | IRON (III) TRANSPORT SYSTEM (PERMEASE). |
| | ID1024 | H | PROBABLE AROMATIC ACID DECARBOXYLASE (EC 4.1.1.-). |
| 15 | ID1025 | H | BH0072 PROTEIN. |
| | ID1026 | H | DGOA PROTEIN [INCLUDES: 2-DEHYDRO-3-DEOXYPHOSPHOGALACTONATE |
| | ID1027 | H | THIAMINE PHOSPHATE PYROPHOSPHORYLASE. |
| | ID1028 | H | CONSERVED HYPOTHETICAL PROTEIN. |
| 20 | ID1029 | H | FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEMESY |
| | ID1030 | H | PROTOPORPHYRINOGEN IX AND COPROPORPHYRINOGEN III OXIDASE. |
| | ID1031 | H | ORF starting with ATG of length 990 |
| 25 | ID1032 | H | MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN C. |
| | ID1033 | H | PROBABLE AMINOTRANSFERASE YHXA (EC 2.6.-.-). |
| | ID1034 | H | ORF starting with ATG of length 624 |
| | ID1035 | H | FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEMESY |
| 30 | ID1036 | H | DIHYDROOPTERIN ALDOLASE (EC 4.1.2.25) (DHNA). |
| | ID1037 | H | FOLATE SYNTHESIS BIFUNCTIONAL PROTEIN [INCLUDES: 2-AMINO-4-H |
| | ID1038 | H | DIHYDROPTEROATE SYNTHASE (DIHYDROPTEROATE PYROPHOSPHORYLASE) |
| 35 | ID1039 | H | SUPEROXIDE-INDUCIBLE PROTEIN. |
| | ID1040 | H | AMIDOTRANSFERASE. |
| | ID1041 | H | ORF starting with ATG of length 267 |
| | ID1042 | H | PANTOATE BETA-ALANINE LIGASE. |
| | ID1043 | H | QUINOLINATE SYNTHETASE. |
| 40 | ID1044 | H | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID1045 | H | GLUTAMATE-1-SEMALDEHYDE 2,1-AMINOTRANSFERASE (EC 5.4.3.8). |
| | ID1046 | H | PHOSPHOMETHYL PYRIMIDINE KINASE (EC 2.7.4.7) (HMP-PHOSPHATE K |
| 45 | ID1047 | H | L-ASPARTATE OXIDASE. |
| | ID1048 | H | FOLYL-POLYGLUTAMATE SYNTHETASE (EC 6.3.2.17). |
| | ID1049 | H | CYTOCHROME CAA3 OXIDASE ASSEMBLY FACTOR. |
| | ID1050 | H | 6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9). |
| | ID1051 | H | PROBABLE 2-DEHYDRO PANTOATE 2-REDUCTASE (EC 1.1.1.169) |
| 50 | (KETOP) | | |
| | ID1052 | H | PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8). |
| | ID1053 | H | GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.). |
| | ID1054 | H | BS PROMOTER (FRAGMENT). |
| | ID1055 | H | GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE. |
| 55 | ID1056 | H | UNKNOWN (PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN). |
| | ID1057 | H | S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE ADEN |
| | ID1058 | H | DIHYDROPTEROATE SYNTHASE (DIHYDROPTEROATE PYROPHOSPHORYLASE) |
| 60 | ID1059 | H | DIHYDROOPTERIN ALDOLASE (EC 4.1.2.25). |
| | ID1060 | H | ORF starting with ATG of length 216 |
| | ID1061 | H | ORF starting with ATG of length 387 |
| | ID1062 | HI | 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE. |
| | ID1063 | HI | Corn 1-deoxy-D-xylulose 5-phosphate synthase putative |
| 65 | protei | | |
| | ID1064 | HR | BH3411 PROTEIN. |

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| | ID1065 | HR | BH3143 PROTEIN. |
| | ID1066 | HR | BH3143 PROTEIN. |
| | ID1067 | HR | BH3411 PROTEIN. |
| 5 | ID1068 | I | PYRUVATE CARBOXYLASE. |
| | ID1069 | I | PROTEIN LOW TEMPERATURE REQUIREMENT C. |
| | ID1070 | I | 3-HYDROXYACYL-COA DEHYDROGENASE. |
| | ID1071 | I | SHORT-CHAIN-SPECIFIC ACYL-COA DEHYDROGENASE. |
| | ID1072 | I | E. coli proliferation associated protein sequence SEQ |
| | ID NO: | | |
| 10 | ID1073 | I | ENOYL- [ACYL-CARRIER PROTEIN] REDUCTASE. |
| | ID1074 | I | ACETYL-COA SYNTHETASE (EC 6.2.1.1). |
| | ID1075 | I | PUTATIVE ACYL CARRIER PROTEIN PHOSPHODIESTERASE (EC |
| | 3.1.4.14 | | |
| 15 | ID1076 | I | ORF starting with ATG of length 341 |
| | ID1077 | I | HYPOTHETICAL 24.9 KDA PROTEIN IN CYTOCHROME P450MEG |
| | GENE 3' R | | |
| | ID1078 | I | FATTY ACID DESATURASE (EC 1.14.99.). |
| | ID1079 | I | FATTY ACID DESATURASE. |
| 20 | ID1080 | I | METHYLMALONYL-COA DECARBOXYLASE, SUBUNIT A LPHA |
| | (MMDA). | | |
| | ID1081 | I | PROBABLE CARDIOLIPIN SYNTHETASE 2 (EC 2.7.8.-) |
| | (CARDIOLIPIN | | |
| | ID1082 | I | BUTYRYL-COA DEHYDROGENASE. |
| 25 | ID1083 | I | ACETYL-COA CARBOXYLASE TRANSFERASE BETA SUBUNIT (EC |
| | 6.4.1.2) | | |
| | ID1084 | I | PROPYONYL-COA CARBOXYLASE. |
| | ID1085 | I | ORF starting with ATG of length 549 |
| | ID1086 | I | ACETYL-COA SYNTHETASE (EC 6.2.1.1). |
| | ID1087 | I | YVAB PROTEIN. |
| 30 | ID1088 | I | PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE. |
| | ID1089 | I | 3-HYDROXYISOBUTYRATE DEHYDROGENASE. |
| | ID1090 | I | ORF starting with ATG of length 561 |
| | ID1091 | I | HYPOTHETICAL 38.4 KDA PROTEIN. |
| | ID1092 | I | LIPASE (ESTERASE). |
| 35 | ID1093 | I | BACITRACIN TRANSPORT PERMEASE PROTEIN BCRC. |
| | ID1094 | I | YWJE PROTEIN. |
| | ID1095 | I | 3-HYDROXYISOBUTYRATE DEHYDROGENASE. |
| | ID1096 | I | ACETYL-COA SYNTHETASE (EC 6.2.1.1). |
| 40 | ID1097 | I | ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9). |
| | ID1098 | I | ACYL-COA DEHYDROGENASE (EC 1.3.99.). |
| | ID1099 | I | ORF starting with ATG of length 600 |
| | ID1100 | I | PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A |
| | TRANSFERASE SUBU | | |
| 45 | ID1101 | I | 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (EC |
| | 1.1.1.-) | | |
| | ID1102 | I | ACETYL-COA CARBOXYLASE BIOTIN CARBOXYLASE SUBUNIT (EC |
| | 6.4.1. | | |
| | ID1103 | I | ACETATE-COA LIGASE. |
| 50 | ID1104 | I | MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC |
| | 2.3.1.39). | | |
| | ID1105 | I | BH1635 PROTEIN. |
| | ID1106 | I | PHOSPHATIDATE CYTIDYLTRANSFERASE. |
| | ID1107 | I | UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31). |
| | ID1108 | I | HYPOTHETICAL 48.2 KDA PROTEIN (FRAGMENT). |
| 55 | ID1109 | I | PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A |
| | TRANSFERASE SUBU | | |
| | ID1110 | I | ORF starting with ATG of length 597 |
| | ID1111 | I | PROBABLE CARDIOLIPIN SYNTHETASE 2 (EC 2.7.8.-) |
| | (CARDIOLIPIN | | |
| 60 | ID1112 | I | HYPOTHETICAL 25.2 KDA PROTEIN. |
| | ID1113 | I | ACETATE-COA LIGASE (EC 6.2.1.1). |
| | ID1114 | I | ACETATE-COA LIGASE. |
| | ID1115 | I | PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE. |
| | ID1116 | I | BIOTIN CARBOXYLASE. |
| 65 | ID1117 | I | BUTYRYL-COA DEHYDROGENASE. |
| | ID1118 | I | BACITRACIN TRANSPORT PERMEASE PROTEIN BCRC. |

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| | ID1119 | I | 3-HYDROXYACYL-COA DEHYDROGENASE. |
| | ID1120 | I | INVOLVED IN FATTY ACID/PHOSPHOLIPID SYNTHESIS. |
| | ID1121 | I | SHORT-CHAIN FATTY ACIDS TRANSPORTER. |
| | ID1122 | I | 3-HYDROXYACYL-COA DEHYDROGENASE. |
| 5 | ID1123 | I | BUTYRYL-COA DEHYDROGENASE. |
| | ID1124 | I | SIMILAR TO PROPIONYL COENZYME A CARBOXYLASE, ALPHA POLYPEPTIDE. |
| | ID1125 | I | PROTEIN LOW TEMPERATURE REQUIREMENT C. |
| | ID1126 | I | ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9). |
| 10 | ID1127 | I | NAD-DEPENDENT BETA-HYDROXYBUTYRYL COENZYME A DEHYDROGENASE. |
| | ID1128 | I | HYPOTHETICAL 18.7 KDA PROTEIN IN HOM-MRGA INTERGENIC REGION. |
| 15 | ID1129 | IQ | LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3) (LONG-CHAIN A). |
| | ID1130 | IQ | LONG-CHAIN FATTY-ACID-COA LIGASE. |
| | ID1131 | IQ | MEDIUM-CHAIN FATTY ACID-COA LIGASE. |
| | ID1132 | IQ | ACID-COA LIGASE. |
| 20 | ID1133 | IQ | ACID-COA LIGASE. |
| | ID1134 | IQ | LONG CHAIN FATTY ACID ACYL-COA LIGASE. |
| | ID1135 | J | BH1439 PROTEIN. |
| | ID1136 | J | VALYL-TRNA SYNTHETASE (EC 6.1.1.9) (VALINE--TRNA LIGASE) (VA). |
| | ID1137 | J | BH1243 PROTEIN. |
| 25 | ID1138 | J | RIBOSOMAL PROTEIN L6 (BL8). |
| | ID1139 | J | RIBOSOMAL PROTEIN L18. |
| | ID1140 | J | RIBOSOMAL PROTEIN S5. |
| | ID1141 | J | Streptococcus pneumoniae prfC protein sequence. |
| | ID1142 | J | METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9). |
| 30 | ID1143 | J | GLYCYL-TRNA SYNTHETASE (ALPHA SUBUNIT). |
| | ID1144 | J | LYSYL-TRNA SYNTHETASE (EC 6.1.1.6). |
| | ID1145 | J | RIBOSOMAL PROTEIN N-ACETYLTRANSFERASE, PUTATIVE. |
| | ID1146 | J | ISOLEUCYL-TRNA SYNTHETASE. |
| | ID1147 | J | BH2847 PROTEIN. |
| 35 | ID1148 | J | ASPARAGINYL-TRNA SYNTHETASE (EC 6.1.1.22) (ASPARAGINE--TRNA). |
| | ID1149 | J | Leucyl-tRNA synthetase from Staph. aureus. |
| | ID1150 | J | ASPARAGINYL-TRNA SYNTHETASE. |
| | ID1151 | J | TRNA PSEUDOURIDINE 5S SYNTHASE. |
| 40 | ID1152 | J | METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9). |
| | ID1153 | J | SA1060 PROTEIN. |
| | ID1154 | J | GLYCYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.14) (GLYCINE--TR). |
| | ID1155 | J | METHIONINE AMINOPEPTIDASE A. |
| 45 | ID1156 | J | RIBOSOMAL PROTEIN S30AE FAMILY. |
| | ID1157 | J | GLYCYL-TRNA SYNTHETASE (BETA SUBUNIT). |
| | ID1158 | J | RRNA METHYLASE. |
| | ID1159 | J | TRYPTOPHANYL-TRNA SYNTHETASE. |
| | ID1160 | J | 16S PSEUDOURIDYLATE SYNTHASE. |
| 50 | ID1161 | J | PUTATIVE TRNA SYNTHETASE. |
| | ID1162 | J | LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4). |
| | ID1163 | J | TRNA/RRNA METHYLTRANSFERASE. |
| | ID1164 | J | HYPOTHETICAL 35.7 KDA PROTEIN IN MALA 3' REGION (ORF3). |
| 55 | ID1165 | J | PROTOPORPHYRINOID OXIDASE. |
| | ID1166 | J | CYSTEINYLYL-TRNA SYNTHETASE (EC 6.1.1.16) (CYSTEINE--TRNA LIGA). |
| | ID1167 | J | ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT (EC 6.1.1.5). |
| 60 | ID1168 | J | TRANSLATION INITIATION INHIBITOR. |
| | ID1169 | J | CYTOSOLIC AXIAL FILAMENT PROTEIN. |
| | ID1170 | J | H. pylori GHP0 728 protein. |
| | ID1171 | J | ORF starting with ATG of length 609. |
| | ID1172 | J | ORF starting with ATG of length 966. |
| 65 | ID1173 | J | THREONYL-TRNA SYNTHETASE 1 (EC 6.1.1.3) (THREONINE--TRNA LIG). |

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| | ID1174 | J | POLY (A) POLYMERASE. |
| | ID1175 | J | ORF starting with ATG of length 543 |
| | ID1176 | J | ASPARTYL-TRNA SYNTHETASE. |
| 5 | ID1177 | J | TRANSLATION INITIATION FACTOR IF-2. |
| | ID1178 | J | ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-- TRNA LIGA |
| | ID1179 | J | HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21). |
| | ID1180 | J | ORF starting with ATG of length 321 |
| 10 | ID1181 | J | TRANSLATION INITIATION FACTOR IF-2. |
| | ID1182 | J | ORF starting with ATG of length 2301 |
| | ID1183 | J | RIBOSOME-BINDING FACTOR A. |
| | ID1184 | J | BH3010 PROTEIN. |
| | ID1185 | J | RIBOSOMAL PROTEIN L27. |
| 15 | ID1186 | J | BH1351 PROTEIN. |
| | ID1187 | J | PROBABLE METHYLTRANSFERASE (EC 2.1.1.-). |
| | ID1188 | J | RIBOSOMAL PROTEIN L27. |
| | ID1189 | J | BH3010 PROTEIN. |
| | ID1190 | J | METHYLTRANSFERASE. |
| 20 | ID1191 | J | LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4). |
| | ID1192 | J | PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.20) (PHENY |
| | ID1193 | J | PSEUDOURIDYLATE SYNTHASE (EC 4.2.1.70). |
| | ID1194 | J | POLY(A) POLYMERASE. |
| 25 | ID1195 | J | POLY(A) POLYMERASE. |
| | ID1196 | J | YFJO PROTEIN. |
| | ID1197 | J | ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-- TRNA LIG |
| | ID1198 | J | BH0299 PROTEIN. |
| 30 | ID1199 | J | TRANSLATION ELONGATION FACTOR G (EF-G). |
| | ID1200 | J | YBXF PROTEIN (RIBOSOMAL PROTEIN L7AE FAMILY). |
| | ID1201 | J | RIBOSOMAL PROTEIN S12. |
| | ID1202 | J | RIBOSOMAL PROTEIN S7 (BS7). |
| | ID1203 | J | ELONGATION FACTOR G (EF-G) (FRAGMENT). |
| 35 | ID1204 | J | TRANSLATION ELONGATION FACTOR G (EF-G). |
| | ID1205 | J | SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (S |
| | ID1206 | J | ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE |
| 40 | ID1207 | J | RNA METHYLTRANSFERASE. |
| | ID1208 | J | GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (|
| | ID1209 | J | Arabidopsis thaliana protein fragment SEQ ID NO: 29871. |
| 45 | ID1210 | J | PROBABLE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT B, MITO |
| | ID1211 | J | GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT B. |
| | ID1212 | J | SERYL-TRNA SYNTHETASE (EC 6.1.1.11). |
| | ID1213 | J | DIMETHYLADENOSE TRANSFERASE (EC 2.1.1.-) (S- |
| | ID1214 | J | ADENOSEYL METHIO |
| 50 | ID1215 | J | RIBONUCLEASE PH (EC 2.7.7.56). |
| | ID1216 | J | HYPOTHETICAL 9.7 KDA PROTEIN IN MFD-DIVIC INTERGENIC REGION. |
| | ID1217 | J | HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-- TRNA LIGA |
| 55 | ID1218 | J | YFLG PROTEIN. |
| | ID1219 | J | YFLG PROTEIN. |
| | ID1220 | J | PUTATIVE METHYLTRANSFERASE (EC 2.1.1.). |
| | ID1221 | J | Enantioselective amidase of Rhodococcus. |
| 60 | ID1222 | J | 50S RIBOSOMAL PROTEIN L30. |
| | ID1223 | J | 50S RIBOSOMAL PROTEIN L15. |
| | ID1224 | J | 50S RIBOSOMAL PROTEIN L15. |
| | ID1225 | J | HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-- TRNA LIGA |
| 65 | ID1226 | J | 30S RIBOSOMAL PROTEIN S19. |
| | ID1227 | J | 50S RIBOSOMAL PROTEIN L22. |
| | | | 30S RIBOSOMAL PROTEIN S17. |

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| | ID1228 | J | 50S RIBOSOMAL PROTEIN L14. |
| | ID1229 | J | 50S RIBOSOMAL PROTEIN L24. |
| | ID1230 | J | 50S RIBOSOMAL PROTEIN L5. |
| 5 | ID1231 | J | ASPARTYL-TRNA SYNTHETASE. |
| | ID1232 | J | 30S RIBOSOMAL PROTEIN S3. |
| | ID1233 | J | 50S RIBOSOMAL PROTEIN L16. |
| | ID1234 | J | CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 (FRAGMENT). |
| | ID1235 | J | 50S RIBOSOMAL PROTEIN L29. |
| | ID1236 | J | PLASMID PMD101 DNA. |
| 10 | ID1237 | J | ORF starting with ATG of length 756 |
| | ID1238 | J | METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10). |
| | ID1239 | J | 30S RIBOSOMAL PROTEIN S17. |
| | ID1240 | J | 50S RIBOSOMAL PROTEIN L14. |
| | ID1241 | J | ARGS. |
| 15 | ID1242 | J | ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19). |
| | ID1243 | J | GLUTAMYL-TRNA SYNTHETASE 1 (EC 6.1.1.17) (GLUTAMATE-- |
| | TRNA LI | | |
| | ID1244 | J | RIBOSOME-BINDING FACTOR A. |
| | ID1245 | J | TRANSLATION INITIATION FACTOR IF-2. |
| 20 | ID1246 | J | HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21). |
| | ID1247 | J | THREONYL-TRNA SYNTHETASE 1 (EC 6.1.1.3). |
| | ID1248 | J | BH2542 PROTEIN. |
| | ID1249 | J | METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10). |
| | ID1250 | J | GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A. |
| 25 | ID1251 | J | TRYPTOPHANYL-TRNA SYNTHETASE. |
| | ID1252 | J | BH1636 PROTEIN. |
| | ID1253 | J | RIBOSOME RECYCLING FACTOR. |
| | ID1254 | J | GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17). |
| 30 | ID1255 | J | 30S RIBOSOMAL PROTEIN S14 HOMOLOG. |
| | ID1256 | J | RIBOSOMAL PROTEIN L17. |
| | ID1257 | J | LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4). |
| | ID1258 | J | RIBOSOMAL PROTEIN S11 (BS11). |
| | ID1259 | J | GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC |
| 35 | 6.3.5.-) (| | |
| | ID1260 | J | GLUTAMYL-TRNA (GLN) AMIDOTRANSFERASE SUBUNIT B. |
| | ID1261 | J | TRYPTOPHANYL-TRNA SYNTHETASE. |
| | ID1262 | J | RIBOSOMAL PROTEIN L28. |
| | ID1263 | J | BH2507 PROTEIN. |
| 40 | ID1264 | J | ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA |
| | LIGASE | | |
| | ID1265 | J | 50S RIBOSOMAL PROTEIN L19. |
| | ID1266 | J | RIBONUCLEASE P PROTEIN COMPONENT (EC 3.1.26.5) |
| | (PROTEIN C5) | | |
| | ID1267 | J | RIBOSOMAL PROTEIN S9 (BS10). |
| 45 | ID1268 | J | GENERAL STRESS PROTEIN. |
| | ID1269 | J | PEPTIDYL-TRNA HYDROLASE. |
| | ID1270 | J | 50S RIBOSOMAL PROTEIN L10. |
| | ID1271 | J | RIBOSOMAL PROTEIN L7/L12. |
| | ID1272 | J | BH0124 PROTEIN. |
| 50 | ID1273 | J | PEPTIDE CHAIN RELEASE FACTOR 2 IN TRANSLATION. |
| | ID1274 | J | RIBOSOMAL PROTEIN L11 (BL11). |
| | ID1275 | J | BH3771 PROTEIN. |
| | ID1276 | J | ORF starting with ATG of length 544 |
| | ID1277 | J | ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT (EC |
| 55 | 6.1.1.5.) (| | |
| | ID1278 | J | THREONYL-TRNA SYNTHETASE 2 (EC 6.1.1.3) (THREONINE-- |
| | TRNA LIG | | |
| | ID1279 | J | PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN (EC |
| 60 | 6.1.1.20) (PHEN | | |
| | ID1280 | J | T9A4.4 PROTEIN. |
| | ID1281 | J | ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT (EC |
| | 6.1.1.5.) (| | |
| | ID1282 | J | ILE-TRNA SYNTHETASE. |
| | ID1283 | J | RNA METHYLTRANSFERASE. |
| 65 | ID1284 | J | BH3085 PROTEIN. |

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| | ID1285 6.1.1.5) (| J | ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT (EC |
| | ID1286 | J | PUTATIVE SERYL-TRNA SYNTHETASE (EC 6.1.1.11). |
| | ID1287 | J | BH0299 PROTEIN. |
| 5 | ID1288 | J | RIBONUCLEASE PH (FRAGMENT). |
| | ID1289 | J | HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21). |
| | ID1290 | J | ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19). |
| | ID1291 | J | PUTATIVE ARGINYL-TRNA SYNTHASE (FRAGMENT). |
| | ID1292 | J | TRNA/RRNA METHYLTRANSFERASE. |
| 10 | ID1293 | J | TRANSLATION ELONGATION FACTOR EF-P. |
| | ID1294 | J | PROLYL-TRNA SYNTHETASE. |
| | ID1295 | J | ORF starting with ATG of length 264 |
| | ID1296 | KE | Brevibacterium lactofermentum aspC protein. |
| | ID1297 | KE | HYPOTHETICAL 46.8 KDA PROTEIN. |
| 15 | ID1298 | KE | YDFD PROTEIN. |
| | ID1299 | KE | Staphylococcus aureus regulator protein. |
| | ID1300 | KE | YDFD PROTEIN. |
| | ID1301 | KE | ORF starting with ATG of length 542 |
| | ID1302 | KE | AMINOTRANSFERASE. |
| 20 | ID1303 | K | TRANSCRIPTIONAL REGULATOR (LACI FAMILY). |
| | ID1304 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1305 | K | TRANSCRIPTIONAL REPRESSOR OF THE TREHALOSE OPERON. |
| | ID1306 | K | ORF starting with ATG of length 565 |
| | ID1307 | K | SUGAR KINASE. |
| 25 | ID1308 | K | BH2511 PROTEIN. |
| | ID1309 | K | STAGE 0 SPORULATION PROTEIN J. |
| | ID1310 HOMOLOG) | K | RIBONUCLEASE R (EC 3.1.-.-) (RNASE R) (VACB PROTEIN |
| 30 | ID1311 CATABOLITE | K | TRANSCRIPTIONAL REGULATOR INVOLVED IN CARBON |
| | ID1312 PROTEIN | CONT | RNA POLYMERASE SIGMA-F FACTOR (STAGE II SPORULATION |
| | ID1313 | K | HYPOTHETICAL PROTEIN TM0326. |
| | ID1314 (TRANSKR | K | DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) |
| 35 | ID1315 OPERON. | K | TRANSCRIPTIONAL ANTITERMINATOR OF GLYCEROL UPTAKE |
| | ID1316 | K | BH0406 PROTEIN. |
| | ID1317 | K | TRANSCRIPTIONAL REGULATOR (LRP/ASNC FAMILY). |
| 40 | ID1318 | K | STAGE 0 SPORULATION PROTEIN J. |
| | ID1319 | K | VIRULENCE-ASSOCIATED PROTEIN. |
| | ID1320 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1321 | K | TRANSCRIPTIONAL REPRESSOR OF THE TREHALOSE OPERON. |
| | ID1322 | K | XYLOSE OPERON REGULATORY PROTEIN (XYLR-2). |
| 45 | ID1323 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1324 | K | BH1706 PROTEIN. |
| | ID1325 | K | PUTATIVE FIBRONECTIN-BINDING PROTEIN (YLOA PROTEIN). |
| | ID1326 | K | PUTATIVE FIBRONECTIN-BINDING PROTEIN (YLOA PROTEIN). |
| | ID1327 | K | TRANSCRIPTIONAL REGULATOR. |
| 50 | ID1328 | K | BH0677 PROTEIN. |
| | ID1329 | K | ORF starting with ATG of length 462 |
| | ID1330 | K | TRANSCRIPTIONAL REGULATOR (MERR FAMILY). |
| | ID1331 | K | TRANSCRIPTIONAL TERMINATOR. |
| | ID1332 | K | ORF starting with ATG of length 585 |
| 55 | ID1333 | K | TRANSCRIPTIONAL REGULATOR (MERR FAMILY). |
| | ID1334 | K | ORF starting with ATG of length 675 |
| | ID1335 | K | TRANSCRIPTIONAL REPRESSOR OF THE XYLOSE OPERON. |
| | ID1336 | K | BH3429 PROTEIN. |
| | ID1337 | K | BH3146 PROTEIN. |
| 60 | ID1338 | K | BH0391 PROTEIN. |
| | ID1339 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1340 | K | ORF starting with ATG of length 573 |
| | ID1341 | K | GLUCOSE KINASE. |
| | ID1342 | K | TRANSCRIPTIONAL REGULATOR. |
| 65 | ID1343 | K | TRANSCRIPTIONAL REGULATOR (LYSR FAMILY). |
| | ID1344 | K | COLD SHOCK PROTEIN CSPC. |

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| | ID1345 | K | ORF starting with ATG of length 624 |
| | ID1346 | K | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID1347 | K | ORF starting with ATG of length 540 |
| | ID1348 | K | TRANSCRIPTIONAL PLEIOTROPIC REGULATOR OF TRANSITION |
| 5 | STATE GE | | |
| | ID1349 | K | YBGA PROTEIN. |
| | ID1350 | K | TRANSCRIPTIONAL PLEIOTROPIC REGULATOR OF TRANSITION |
| | STATE GE | | |
| 10 | ID1351 | K | STAGE V SPORULATION PROTEIN T. |
| | ID1352 | K | HYPOTHETICAL 29.9 KDA PROTEIN. |
| | ID1353 | K | ORF starting with ATG of length 504 |
| | ID1354 | K | HYPOTHETICAL 26.2 KDA PROTEIN IN FTSH-CYSK INTERGENIC |
| | REGION | | |
| 15 | ID1355 | K | TRANSCRIPTIONAL REGULATOR (ARAC/XYLS FAMILY). |
| | ID1356 | K | VIRULENCE-ASSOCIATED PROTEIN. |
| | ID1357 | K | VIRULENCE-ASSOCIATED PROTEIN. |
| | ID1358 | K | TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY). |
| | ID1359 | K | BH0655 PROTEIN. |
| | ID1360 | K | TRANSCRIPTIONAL REGULATOR INVOLVED IN CARBON |
| 20 | CATABOLITE CONT | | |
| | ID1361 | K | TRANSCRIPTIONAL REGULATOR (HEX REGULON REPRESSOR). |
| | ID1362 | K | TRANSCRIPTIONAL REGULATOR (MERR FAMILY). |
| | ID1363 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1364 | K | HYPOTHETICAL 13.3 KDA PROTEIN. |
| 25 | ID1365 | K | MLL3592 PROTEIN. |
| | ID1366 | K | TRANSCRIPTIONAL REGULATOR (LYSR FAMILY). |
| | ID1367 | K | MLL3592 PROTEIN. |
| | ID1368 | K | RNA POLYMERASE SIGMA-54 FACTOR. |
| | ID1369 | K | TRANSCRIPTIONAL REGULATOR. |
| 30 | ID1370 | K | TRANSCRIPTIONAL REGULATOR (LACI FAMILY). |
| | ID1371 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1372 | K | ORF starting with ATG of length 375 |
| | ID1373 | K | ORF starting with ATG of length 225 |
| | ID1374 | K | RNA POLYMERASE GENERAL STRESS SIGMA FACTOR (SIGMA B). |
| 35 | ID1375 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN COTF-TETB |
| | INTERGEN | | |
| | ID1376 | K | PUTATIVE GNTR-FAMILY TRANSCRIPTIONAL REGULATOR. |
| | ID1377 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1378 | K | RNA POLYMERASE SIGMA FACTOR (SIGMA54). |
| 40 | ID1379 | K | RNA POLYMERASE SIGMA-D FACTOR. |
| | ID1380 | K | TRANSCRIPTIONAL FACTOR. |
| | ID1381 | K | TRANSCRIPTION REGULATOR. |
| | ID1382 | K | PROBABLE HTH_ARAC_FAMILY OF TRANSCRIPTIONAL |
| | REGULATOR. | | |
| 45 | ID1383 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YRAN. |
| | ID1384 | K | BH0317 PROTEIN. |
| | ID1385 | K | DNA-DIRECTED RNA POLYMERASE BETA SUBUNIT (EC |
| | 2.7.7.6). | | |
| | ID1386 | K | RNA POLYMERASE BETA SUBUNIT. |
| 50 | ID1387 | K | ORF starting with ATG of length 603 |
| | ID1388 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1389 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1390 | K | PUTATIVE TRANSCRIPTIONAL REGULATOR (TRANSCRIPTIONAL |
| | REGULATO | | |
| 55 | ID1391 | K | ORF starting with ATG of length 312 |
| | ID1392 | K | TRANSCRIPTIONAL TERMINATOR. |
| | ID1393 | K | RNA POLYMERASE SIGMA FACTOR (SIGMA K) PRECURSOR. |
| | ID1394 | K | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID1395 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| 60 | ID1396 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1397 | K | STAGE V SPORULATION PROTEIN T. |
| | ID1398 | K | TRANSCRIPTIONAL REGULATOR, LACI FAMILY. |
| | ID1399 | K | TRANSCRIPTIONAL REGULATOR INVOLVED IN CARBON |
| | CATABOLITE CONT | | |
| 65 | ID1400 | K | PURR. |

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| | ID1401 (TRANSCR | K | DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) |
| | ID1402 | K | PROTEASE PRODUCTION REGULATORY PROTEIN HPR. |
| | ID1403 | K | DNA-DIRECTED RNA POLYMERASE DELTA SUBUNIT (EC |
| 5 | 2.7.7.6). | | |
| | ID1404 | K | PUTATIVE SUCROSE OPERON REPRESSOR. |
| | ID1405 | K | ORF starting with ATG of length 513 |
| | ID1406 | K | SIMILAR TO B. SUBTILIS YWGB GENE (BH0656 PROTEIN). |
| | ID1407 | K | FIBRONECTIN/FIBRINOGEN-BINDING PROTEIN. |
| 10 | ID1408 2.7.7.6). | K | DNA-DIRECTED RNA POLYMERASE ALPHA SUBUNIT (EC |
| | ID1409 2.7.7.6). | K | DNA-DIRECTED RNA POLYMERASE ALPHA SUBUNIT (EC |
| 15 | ID1410 | K | RNA POLYMERASE GENERAL STRESS SIGMA FACTOR (SIGMA B). |
| | ID1411 | K | RIBONUCLEASE III. |
| | ID1412 | K | BH3951 PROTEIN. |
| | ID1413 | K | YOZA PROTEIN. |
| | ID1414 OPERON (| K | TRANSCRIPTIONAL ACTIVATOR OF THE GLUTAMATE SYNTHASE |
| 20 | ID1415 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1416 | K | TRANSCRIPTIONAL ELONGATION FACTOR. |
| | ID1417 | K | ORF starting with ATG of length 599 |
| | ID1418 | K | ORF starting with ATG of length 600 |
| | ID1419 | K | CATABOLITE CONTROL PROTEIN A. |
| 25 | ID1420 | K | ORF starting with ATG of length 461 |
| | ID1421 | K | METHICILLIN RESISTANCE PROTEIN MECI. |
| | ID1422 | K | HYPOTHETICAL PROTEIN. |
| | ID1423 | K | DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) |
| 30 | ID1424 (TRANSCR | K | BH0406 PROTEIN. |
| | ID1425 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1426 | K | COLD SHOCK PROTEIN CSPC. |
| | ID1427 | K | YDEB PROTEIN (ORFC). |
| | ID1428 | K | ORF starting with ATG of length 663 |
| 35 | ID1429 | K | TRANSCRIPTIONAL REGULATOR (LRP/ASNC FAMILY). |
| | ID1430 | K | HYPOTHETICAL 21.8 KDA PROTEIN YVBF (ORF1). |
| | ID1431 | K | HYPOTHETICAL 31.6 KDA PROTEIN. |
| | ID1432 | K | ORF starting with ATG of length 582 |
| | ID1433 | K | YVNA. |
| 40 | ID1434 | K | TRANSCRIPTIONAL REGULATOR (ARAC/XYLS FAMILY). |
| | ID1435 | K | TRANSCRIPTIONAL REGULATOR INVOLVED IN CARBON |
| | CATABOLITE CONT | | |
| | ID1436 | K | TRANSCRIPTIONAL REGULATOR OF EXTRACELLULAR ENZYME |
| | GENES. | | |
| 45 | ID1437 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1438 (TRANSC | K | DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2.7.7.6) |
| | ID1439 (TRANSC | K | DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2.7.7.6) |
| 50 | ID1440 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID1441 | K | TRANSCRIPTIONAL REPRESSOR OF THE TREHALOSE OPERON. |
| | ID1442 | K | STAGE 0 SPORULATION PROTEIN J. |
| | ID1443 | K | DNA-BINDING PROTEIN SPO0J-LIKE HOMOLOG. |
| | ID1444 | K | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| 55 | ID1445 | K | ORF starting with ATG of length 642 |
| | ID1446 | K | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YKUM. |
| | ID1447 | K | RNA POLYMERASE SIGMA FACTOR (SIGMA54). |
| | ID1448 | K | TRANSCRIPTIONAL REGULATOR (LACI FAMILY). |
| | ID1449 | K | TRANSCRIPTIONAL REGULATOR (MARR FAMILY). |
| 60 | ID1450 | K | ORF starting with ATG of length 603 |
| | ID1451 | K | TRANSCRIPTIONAL REGULATOR. |
| | ID1452 PROTEIN | KG | PUTATIVE LACTOSE PHOSPHOTRANSFERASE SYSTEM REPRESSOR |
| | ID1453 | KG | YTZE PROTEIN. |
| 65 | ID1454 | KG | ORF starting with ATG of length 792 |
| | ID1455 | KG | TRANSCRIPTIONAL REGULATOR (DEOR FAMILY). |

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| | ID1456 | KG | DNA-BINDING PROTEIN IOLR. |
| | ID1457 | KL | SNF2 HELICASE. |
| | ID1458 | KL | SNF2 HELICASE. |
| 5 | ID1459 | KL | ORF starting with ATG of length 489 |
| | ID1460 | KL | HELICASE (SNF2/RAD54 FAMILY). |
| | ID1461 | KL | HELICASE (SNF2/RAD54 FAMILY). |
| | ID1462 | KL | SNF2 HELICASE. |
| | ID1463 | KL | SNF2 HELICASE. |
| 10 | ID1464 | KR | BH1438 PROTEIN. |
| | ID1465 | KR | BH0466 PROTEIN. |
| | ID1466 | KR | BH2157 PROTEIN. |
| | ID1467 | KR | BH2157 PROTEIN. |
| | ID1468 | KR | Protease gene expression protein. |
| | ID1469 | KR | ACETYLTRANSFERASE, PUTATIVE. |
| 15 | ID1470 | KR | BH0478 PROTEIN. |
| | ID1471 | KT | TRANSCRIPTIONAL REPRESSOR OF THE SOS REGULON. |
| | ID1472 | KT | TRANSCRIPTIONAL REPRESSOR OF THE SOS REGULON. |
| | ID1473 | L | DNA GYRASE SUBUNIT A (EC 5.99.1.3). |
| 20 | ID1474 | L | RECF PROTEIN (DNA REPAIR AND GENETIC RECOMBINATION). |
| | ID1475 | L | ORF starting with TTG or GTG of length 557 |
| | ID1476 | L | PRIMOSOMAL REPLICATION FACTOR Y. |
| | ID1477 | L | PRIMOSOMAL REPLICATION FACTOR Y. |
| | ID1478 | L | TRANSPOSAE (09). |
| 25 | ID1479 | L | YQV PROTEIN. |
| | ID1480 | L | TRANSPOSAE (08). |
| | ID1481 | L | EXCINUCLEASE ABC (SUBUNIT C). |
| | ID1482 | L | DNA POLYMERASE III ALPHA SUBUNIT (EC 2.7.7.7). |
| | ID1483 | L | PUTATIVE TRANSPOSAE. |
| 30 | ID1484 | L | DNA TOPOISOMERASE IV SUBUNIT A. |
| | ID1485 | L | ORF starting with ATG of length 426 |
| | ID1486 | L | PRIMOSOMAL REPLICATION FACTOR Y. |
| | ID1487 | L | DNA-DEPENDENT DNA POLYMERASE BETA CHAIN. |
| | ID1488 | L | TRANSPOSAE. |
| | ID1489 | L | HYPOTHETICAL 60.7 KDA PROTEIN. |
| 35 | ID1490 | L | TRANSPOSAE (10). |
| | ID1491 | L | BH2209 PROTEIN. |
| | ID1492 | L | PUTATIVE 3-METHYLADENINE DNA GLYCOSYLASE (EC 3.2.2.-). |
| | ID1493 | L | HYPOTHETICAL 45.9 KDA PROTEIN IN GLNQ-ANSR INTERGENIC |
| 40 | REGION | | |
| | ID1494 | L | ATP/GTP-BINDING PROTEIN (IMPB/MUCB/SAMB FAMILY). |
| | ID1495 | L | DNA PRIMASE. |
| | ID1496 | L | DNA TOPOISOMERASE IV SUBUNIT B. |
| 45 | ID1497 | L | DNA MISMATCH REPAIR PROTEIN (MISMATCH RECOGNITION STEP). |
| | ID1498 | L | DNA MISMATCH REPAIR PROTEIN. |
| | ID1499 | L | EXODEOXYRIBONUCLEASE VII (SMALL SUBUNIT). |
| | ID1500 | L | PUTATIVE TRANSPOSAE. |
| | ID1501 | L | ORF starting with ATG of length 615 |
| 50 | ID1502 | L | BH4041 PROTEIN. |
| | ID1503 | L | YKFC PROTEIN. |
| | ID1504 | L | EXODEOXYRIBONUCLEASE VII (LARGE SUBUNIT). |
| | ID1505 | L | TRANSPOSAE (09). |
| | ID1506 | L | METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1). |
| 55 | ID1507 | L | EXCINUCLEASE ABC (SUBUNIT B). |
| | ID1508 | L | ENDONUCLEASE-LIKE PROTEIN. |
| | ID1509 | L | PUTATIVE TRANSPOSAE. |
| | ID1510 | L | DNAX, YAAK, RECR, YAAL, BOFA, RRNB-16S, RRNB-23S, |
| 60 | RRNB-5S, O | | |
| | ID1511 | L | PRIMOSOME COMPONENT (HELICASE LOADER). |
| | ID1512 | L | TYPE I RESTRICTION ENZYME STYSP1 M PROTEIN (EC 2.1.1.72) (M. |
| | ID1513 | L | TYPE I RESTRICTION ENZYME ECOKI R PROTEIN (EC 3.1.21.3) (R.E) |
| 65 | ID1514 | L | ORF starting with ATG of length 693 |

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| | ID1515 | L | TRANSPOSAE (08). |
| | ID1516 | L | EXCINUCLEASE ABC (SUBUNIT A). |
| | ID1517 | L | DNA MISMATCH REPAIR PROTEIN MUTL. |
| | ID1518 | L | YRRC PROTEIN. |
| 5 | ID1519 | L | DNA GYRASE SUBUNIT B (EC 5.99.1.3). |
| | ID1520 | L | DNA GYRASE SUBUNIT A (EC 5.99.1.3). |
| | ID1521 | L | PROBABLE ENDONUCLEASE IV (FRAGMENT). |
| | ID1522 | L | FORMAMIDOPYRIMIDINE-DNA GLYCOSIDASE (EC 3.2.2.23). |
| | ID1523 | L | STRESS-AND STARVATION-INDUCED GENE CONTROLLED BY |
| 10 | SIGMA-B. | | |
| | ID1524 | L | HOLLIDAY JUNCTION DNA HELICASE. |
| | ID1525 | L | YLBH PROTEIN. |
| | ID1526 | L | EXCINUCLEASE ABC (SUBUNIT A). |
| 15 | ID1527 | L | PROBABLE DNA TOPOISOMERASE III (EC 5.99.1.2) |
| | (RELAXING ENZYM | | PROBABLE DNA TOPOISOMERASE III (EC 5.99.1.2) |
| | ID1528 | L | |
| | (RELAXING ENZYM | | |
| | ID1529 | L | YVGS PROTEIN. |
| | ID1530 | L | BH4041 PROTEIN. |
| 20 | ID1531 | L | INTEGRASE/RECOMBINASE. |
| | ID1532 | L | TRANSPOSAE (09). |
| | ID1533 | L | DNA POLYMERASE III ALPHA SUBUNIT (EC 2.7.7.7). |
| | ID1534 | L | DNA POLYMERASE III ALPHA SUBUNIT (EC 2.7.7.7). |
| | ID1535 | L | PUTATIVE DNA POLYMERASE III , ALPHA SUBUNIT (DNA |
| 25 | POLYMERASE | | |
| | ID1536 | L | HYPOTHETICAL 17.0 KDA PROTEIN. |
| | ID1537 | L | DNA GYRASE SUBUNIT A (EC 5.99.1.3). |
| | ID1538 | L | HYPOTHETICAL PROTEIN IN TETL 3'REGION (FRAGMENT). |
| | ID1539 | L | RESTRICTION MODIFICATION ENZYME. |
| 30 | ID1540 | L | TRANSPOSAE (23). |
| | ID1541 | L | TRANSPOSAE. |
| | ID1542 | L | Potential <i>M. capsulatus</i> transposase. |
| | ID1543 | L | PXO1-18. |
| 35 | ID1544 | L | TRANSPOSAE. |
| | ID1545 | L | DNA MISMATCH REPAIR PROTEIN. |
| | ID1546 | L | ORF starting with ATG of length 366 |
| | ID1547 | L | HYPOTHETICAL 20.7 KDA PROTEIN IN METS-KSGA INTERGENIC |
| | REGION | | |
| | ID1548 | L | ATP-DEPENDENT DNA HELICASE. |
| 40 | ID1549 | L | ORF starting with ATG of length 629 |
| | ID1550 | L | RIBONUCLEASE HII (EC 3.1.26.4) (RNASE HII). |
| | ID1551 | L | DNA POLYMERASE III SUBUNIT GAMMA/TAU (EC 2.7.7.7). |
| | ID1552 | L | COME OPERON PROTEIN 1. |
| | ID1553 | L | DNA POLYMERASE III GAMMA AND TAU SUBUNITS (EC |
| 45 | 2.7.7.7). | | |
| | ID1554 | L | DNA REPAIR PROTEIN UVRA. |
| | ID1555 | L | EXCINUCLEASE ABC (SUBUNIT B). |
| | ID1556 | L | EXCINUCLEASE ABC (SUBUNIT A). |
| | ID1557 | L | BH3832 PROTEIN. |
| 50 | ID1558 | L | ATP-DEPENDENT DNA HELICASE. |
| | ID1559 | L | <i>Streptomyces globisporus</i> C-1027 gene cluster ORF -1. |
| | ID1560 | L | ATP-DEPENDENT DNA HELICASE. |
| | ID1561 | L | YVGS PROTEIN. |
| | ID1562 | L | EXODEOXYRIBONUCLEASE (EC 3.1.11.2). |
| 55 | ID1563 | L | INT459. |
| | ID1564 | L | DNA REPAIR AND GENETIC RECOMBINATION. |
| | ID1565 | L | BH2382 PROTEIN. |
| | ID1566 | L | DNA REPAIR AND GENETIC RECOMBINATION. |
| | ID1567 | L | RESTRICTION ENDONUCLEASE. |
| 60 | ID1568 | L | SINGLE-STRAND DNA-SPECIFIC EXONUCLEASE. |
| | ID1569 | L | DNA POLYMERASE III, DELTA' SUBUNIT (EC 2.7.7.7). |
| | ID1570 | L | 5'-3' EXONUCLEASE. |
| | ID1571 | L | 5'-3' EXONUCLEASE. |
| | ID1572 | L | ATP-DEPENDENT DNA HELICASE. |
| 65 | ID1573 | L | TYPE I RESTRICTION-MODIFICATION SYSTEM SPECIFICITY |
| | DETERMINA | | |

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| | ID1574 | L | DNA POLYMERASE I (EC 2.7.7.7). |
| | ID1575 | L | FORMAMIDOPYRIMIDINE-DNA GLYCOSIDASE (EC 3.2.2.23). |
| | ID1576 | L | DNA POLYMERASE I (EC 2.7.7.7). |
| | ID1577 | L | BH1765 PROTEIN. |
| 5 | ID1578 | L | SPORE PHOTOPRODUCT LYASE (EC 4.1.99.-). |
| | ID1579 | L | ATP-DEPENDENT DNA HELICASE. |
| | ID1580 | L | DNA GYRASE SUBUNIT A (EC 5.99.1.3). |
| | ID1581 | L | ORF starting with ATG of length 426 |
| | ID1582 | L | TRANSPOSSASE-IS1562. |
| 10 | ID1583 | L | TYPE I RESTRICTION ENZYME ECOKI R PROTEIN (EC 3.1.21.3) (R.E) |
| | ID1584 | L | 5'-3' EXONUCLEASE. |
| | ID1585 | L | DNA-3-METHYLADENINE GLYCOSYLASE (EC 3.2.2.21) (3-METHYLADENINE) |
| 15 | ID1586 | L | DNA POLYMERASE III (ALPHA SUBUNIT). |
| | ID1587 | L | HELICASE IV (EC 3.6.1.-) (75 KDA HELICASE). |
| | ID1588 | L | DNA POLYMERASE III (ALPHA SUBUNIT). |
| | ID1589 | L | TYPE I RESTRICTION ENZYME ECOKI R PROTEIN (EC 3.1.21.3) (R.E) |
| 20 | ID1590 | L | METHYLTRANSFERASE. |
| | ID1591 | L | BH1269 PROTEIN. |
| | ID1592 | L | EXCINUCLEASE ABC (SUBUNIT B). |
| | ID1593 | L | DNAH PROTEIN (DNA POLYMERASE III) (BETA SUBUNIT). |
| | ID1594 | L | RECF PROTEIN (DNA REPAIR AND GENETIC RECOMBINATION). |
| 25 | ID1595 | L | DNA GYRASE SUBUNIT B (EC 5.99.1.3). |
| | ID1596 | L | A gyrase protein sequence. |
| | ID1597 | L | TRANSPOSSASE (27). |
| | ID1598 | L | DNA MISMATCH REPAIR PROTEIN. |
| | ID1599 | L | TRANSPOSSASE (09). |
| 30 | ID1600 | L | CASSETTE CHROMOSOME RECOMBINASE B1. |
| | ID1601 | L | TOPOISOMERASE IV SUBUNIT A (EC 5.99.1.-). |
| | ID1602 | L | ATP-DEPENDENT DNA HELICASE RECQ (EC 3.6.1.-). |
| | ID1603 | L | ATP-DEPENDENT DNA HELICASE RECQ. |
| | ID1604 | L | TRANSPOSSASE (10). |
| 35 | ID1605 | L | HYPOTHETICAL 17.0 KDA PROTEIN. |
| | ID1606 | L | DNA MISMATCH REPAIR PROTEIN (MISMATCH RECOGNITION STEP). |
| | ID1607 | L | DNA MISMATCH REPAIR PROTEIN. |
| | ID1608 | L | DNA MISMATCH REPAIR PROTEIN (MISMATCH RECOGNITION STEP). |
| 40 | ID1609 | L | ORF starting with ATG of length 468 |
| | ID1610 | L | TRANSPOSSASE. |
| | ID1611 | L | TRANSPOSSASE (08). |
| | ID1612 | L | STRESS-AND STARVATION-INDUCED GENE CONTROLLED BY SIGMA-B. |
| 45 | ID1613 | L | HYPOTHETICAL 17.0 KDA PROTEIN. |
| | ID1614 | L | PUTATIVE TRANSPOSSASE. |
| | ID1615 | L | PXO1-120. |
| | ID1616 | L | ORF starting with ATG of length 1380 |
| 50 | ID1617 | L | RIBONUCLEASE HII (EC 3.1.26.4) (RNASE HII). |
| | ID1618 | L | YVGS PROTEIN. |
| | ID1619 | L | CASSETTE CHROMOSOME RECOMBINASE B1. |
| | ID1620 | L | BH3609 PROTEIN. |
| | ID1621 | L | DNA-3-METHYLADENINE GLYCOSYLASE (EC 3.2.2.21) (3-METHYLADENINE) |
| 55 | ID1622 | L | DNA REPAIR PROTEIN. |
| | ID1623 | LK | TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF). |
| | ID1624 | LK | ATP-DEPENDENT DNA HELICASE (EC 3.6.1.). |
| | ID1625 | LK | ATP-DEPENDENT DNA HELICASE (EC 3.6.1.). |
| 60 | ID1626 | LK | TRANSCRIPTION-REPAIR COUPLING FACTOR. |
| | ID1627 | LKJ | ATP-DEPENDENT RNA HELICASE. |
| | ID1628 | LKJ | ATP-DEPENDENT RNA HELICASE. |
| | ID1629 | LKJ | ATP-DEPENDENT RNA HELICASE. |
| | ID1630 | LKJ | LATE COMPETENCE PROTEIN. |
| 65 | ID1631 | LR | MUTATOR MUTT PROTEIN. |
| | ID1632 | LR | BH0986 PROTEIN. |

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| | ID1633 | LR | ORF10291-1 (FRAGMENT). |
| | ID1634 | LR | BH1281 PROTEIN. |
| | ID1635 | M | HYPOTHETICAL 73.2 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| 5 | ID1636 carboxypep | M | S. fradiae tylosin biosynthetic pathway D-alanine |
| | ID1637 D-ALANIN | M | PENICILLIN-BINDING PROTEIN DACF PRECURSOR (D-ALANYL- |
| | ID1638 | M | UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTTRANSFERASE (EC |
| 10 | 2.5.1. | | |
| | ID1639 | M | ORF starting with ATG of length 882 |
| | ID1640 | M | CELL-SHAPE DETERMINING PROTEIN. |
| | ID1641 | M | GLYCINE BETAINE TRANSPORTER. |
| | ID1642 | M | CELL-SHAPE DETERMINING PROTEIN. |
| 15 | ID1643 pASK46. | M | Sequence translated from reading frame b of plasmid |
| | ID1644 such as i | M | autolysin useful in degrading bacterial cell walls |
| | ID1645 | M | N-ACETYLMURAMOYL-L-ALANINE AMIDASE. |
| 20 | ID1646 | M | ORF starting with ATG of length 360 |
| | ID1647 | M | PENICILLIN-BINDING PROTEINS 1A/1B. |
| | ID1648 | M | ORF starting with ATG of length 537 |
| | ID1649 | M | PENICILLIN-BINDING PROTEIN 2A (SPORE OUTGROWTH). |
| | ID1650 | M | S. aureus MurB protein #1. |
| 25 | ID1651 | M | DNAG, RPOD, CPOA GENES AND ORF3 AND ORF5 (FRAGMENT). |
| | ID1652 (GALACTOWALDENASE) | M | UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) |
| | ID1653 | M | UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC |
| 30 | 2.7.7.23). | | |
| | ID1654 | M | GCPE PROTEIN HOMOLOG. |
| | ID1655 | M | BETA-LACTAMASE III PRECURSOR (EC 3.5.2.6). |
| | ID1656 | M | PENICILLIN-BINDING PROTEIN 3 (PBP 3) (PSPB20). |
| | ID1657 | M | B. subtilis hexulose phosphate synthase. |
| | ID1658 ALANINEC | M | PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D- |
| 35 | ID1659 | M | YKFC. |
| | ID1660 | M | S. aureus gidB protein sequence. |
| | ID1661 | M | B. stearothermophilus alanine racemase. |
| | ID1662 | M | HYPOTHETICAL 20.0 KDA PROTEIN IN TLPC-SRFAA |
| 40 | INTERGENIC REGIO | | |
| | ID1663 | M | BH1683 PROTEIN. |
| | ID1664 | M | UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC |
| 2.7.7.23). | | | |
| | ID1665 | M | YRVJ PROTEIN. |
| 45 | ID1666 | M | SUBSTRATE BINDING PROTEIN OPUCC. |
| | ID1667 (GALACTOWALDENASE) | M | UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) |
| | ID1668 | M | UDP PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A). |
| | ID1669 | M | OUTER MEMBRANE LIPOPROTEIN GNA1946. |
| 50 | ID1670 | M | BH1683 PROTEIN. |
| | ID1671 such as i | M | autolysin useful in degrading bacterial cell walls |
| | ID1672 | M | PENICILLIN-BINDING PROTEIN 1A (GERMINATION). |
| | ID1673 | M | ORF starting with ATG of length 453 |
| 55 | ID1674 | M | PENICILLIN-BINDING PROTEIN 1A (GERMINATION). |
| | ID1675 | M | PENICILLIN-BINDING PROTEINS 1A/1B. |
| | ID1676 | M | CELL WALL-BINDING PROTEIN. |
| | ID1677 | M | PENICILLIN-BINDING PROTEIN 1A. |
| | ID1678 | M | HYPOTHETICAL 20.0 KDA PROTEIN IN TLPC-SRFAA |
| 60 | INTERGENIC REGIO | | |
| | ID1679 | M | PENICILLIN-BINDING PROTEIN 1A. |
| | ID1680 | M | D-ALANINE-D-ALANINE LIGASE A. |
| | ID1681 | M | PUTATIVE D-ALANINE:D-ALANINE LIGASE (DDL) (FRAGMENT). |
| | ID1682 | M | HYPOTHETICAL 42.0 KDA PROTEIN IN DAPB-PAPS INTERGENIC |
| 65 | REGION | | |
| | ID1683 | M | PENICILLIN-BINDING PROTEIN. |

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| | ID1684 | M | CSBB PROTEIN. |
| | ID1685 | M | UDP-N-ACETYLMURAMATE-ALANINE LIGASE (EC 6.3.2.8). |
| | ID1686 | M | PUTATIVE GLYCOSYLTRANSFERASE (FRAGMENT). |
| | ID1687 | M | PENICILLIN-BINDING PROTEIN 2B (CELL-DIVISION SEPTUM). |
| 5 | ID1688 | M | D-ALANINE--D-ALANINE LIGASE A (EC 6.3.2.4) (D- |
| | <u>ALANYLALANINES</u> | | |
| | ID1689 | M | STAGE V SPORULATION PROTEIN (SOPRULATION SPECIFIC |
| | PENICILLIN | | |
| 10 | ID1690 | M | SIMILAR TO PSEUDOMONAS AERUGINOSA GDP-MANNOSE 6- |
| | <u>DEHYDROGENAS</u> | | |
| | ID1691 | M | TUAG PROTEIN. |
| | ID1692 | M | UDP-GLUCOSE 6-DEHYDROGENASE. |
| | ID1693 | M | BH2420 PROTEIN. |
| 15 | ID1694 | M | YFNI. |
| | ID1695 | M | TUAG PROTEIN. |
| | ID1696 | M | DNAG, RPOD, CPOA GENES AND ORF3 AND ORF5. |
| | ID1697 | M | SPORE CORTEX-LYTIC ENZYME. |
| | ID1698 | M | BH1391 PROTEIN. |
| 20 | ID1699 | M | PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99.). |
| | ID1700 | M | PUTATIVE PENICILLIN BINDING PROTEIN PRECURSOR. |
| | ID1701 | M | PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99.). |
| 25 | ID1702 | M | STAGE V SPORULATION PROTEIN (SOPRULATION SPECIFIC |
| | PENICILLIN | | |
| | ID1703 | M | UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2, 6- |
| | <u>DIAMINOPIMELATE L</u> | | |
| | ID1704 | M | STAGE II SPORULATION PROTEIN. |
| 30 | ID1705 | M | D-ALANINE-D-ALANINE LIGASE A. |
| | ID1706 | M | UDP-N-ACETYLGLUCOSAMINE-LIKE PROTEIN. |
| | ID1707 | M | UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1. |
| | ID1708 | M | BH3436 PROTEIN. |
| 35 | ID1709 | M | TEICHOIC ACID BIOSYNTHESIS PROTEIN. |
| | ID1710 | M | TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG. |
| | ID1711 | M | TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG. |
| | ID1712 | M | UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9) (U |
| 40 | ID1713 | M | N-ACETYLMURAMOYL-L-ALANINE AMIDASE (MAJOR AUTOLYSIN). |
| | ID1714 | M | LIPOPOLYSACCHARIDE BIOSYNTHESIS PROTEIN. |
| | ID1715 | M | INTERCOMPARTMENTAL SIGNALLING OF PRO-SIGMA-K |
| | <u>PROCESSING/ACTI</u> | | |
| | ID1716 | M | UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9) (U |
| 45 | ID1717 | M | GLYCINE BETAINE TRANSPORTER BETL. |
| | ID1718 | M | Racillus subtilis teichoic acid polymerase. |
| | ID1719 | M | HYPOTHETICAL 73.2 KDA PROTEIN IN SODA-COMGA |
| | <u>INTERGENIC REGIO</u> | | |
| | ID1720 | M | LYTIC TRANSGLYCOSYLASE. |
| 50 | ID1721 | M | ORF starting with ATG of length 894 |
| | ID1722 | M | PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PBP 4). |
| | ID1723 | M | PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PBP 4). |
| | ID1724 | M | BH3268 PROTEIN. |
| | ID1725 | M | UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE (EC 6.3.2.9) |
| 55 | ID1726 | M | Racillus subtilis teichoic acid polymerase. |
| | ID1727 | M | MRAW PROTEIN (YLLC PROTEIN). |
| | ID1728 | M | ORF starting with ATG of length 459 |
| | ID1729 | M | PENICILLIN-BINDING PROTEIN 2B (CELL-DIVISION SEPTUM). |
| 60 | ID1730 | M | S. pneumoniae derived protein #264. |
| | ID1731 | M | PUTATIVE GLYCOSYLTRANSFERASE. |
| | ID1732 | M | BH3436 PROTEIN. |
| | ID1733 | M | ORF starting with ATG of length 888 |
| | ID1734 | M | BH2666 PROTEIN. |
| 65 | ID1735 | M | Staphylococcus aureus protein SEQ ID #5196. |

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| | ID1736 | M | L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE (EC 2.6.) |
| | ID1737 | M | CELL-SHAPE DETERMINING PROTEIN. |
| 5 | ID1738 | M | ORF starting with ATG of length 438 |
| | ID1739 | M | S. aureus gidB protein sequence. |
| | ID1740 | M | S. aureus MurB protein SEQ ID 1. |
| | ID1741 | M | GLYCINE BETAINE/CARNITINE/CHOLINE ABC TRANSPORTER (OSMOPROTE |
| 10 | ID1742 | M | TEICHOIC ACID BIOSYNTHESIS PROTEIN F. |
| | ID1743 | M | PENICILLIN-BINDING PROTEIN 2B (CELL-DIVISION SEPTUM). |
| | ID1744 | M | PROTEOPHOSPHOGLYCAN PRECURSOR (FRAGMENT). |
| | ID1745 | M | STAGE V SPORULATION PROTEIN (SOPRULATION SPECIFIC |
| | PENICILLIN | | |
| 15 | ID1746 | M | PUTATIVE UNDECAPRENYL-PHOSPHATE N- |
| | ACETYLGLUCOSAMINYLTRANSFER | | |
| | ID1747 | M | CELL-DIVISION INITIATION PROTEIN (SEPTUM FORMATION). |
| | ID1748 | M | DNAG, RPOD, CPOA GENES AND ORF3 AND ORF5 (FRAGMENT). |
| | ID1749 | MG | GDP-D-MANNOSE DEHYDRATASE. |
| 20 | ID1750 | MG | PROBABLE EPIMERASE. |
| | ID1751 | MG | HYPOTHETICAL 22.8 KDA PROTEIN. |
| | ID1752 | MI | GCT. |
| | ID1753 | MJ | GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE. |
| | ID1754 | MJ | GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE. |
| 25 | ID1755 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPA. |
| | ID1756 | N | HYPOTHETICAL LIPOPROTEIN YUFN PRECURSOR. |
| | ID1757 | N | BH0721 PROTEIN. |
| | ID1758 | N | SIGNAL PEPTIDASE I (EC 3.4.21.89) (SPASE I) (LEADER |
| | PEPTIDAS | | |
| 30 | ID1759 | N | ORF starting with ATG of length 819 |
| | ID1760 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN. |
| | ID1761 | N | PREPROTEIN TRANSLOCASE SUBUNIT. |
| | ID1762 | N | ORF starting with ATG of length 693 |
| | ID1763 | N | PREPROTEIN TRANSLOCASE, SECA. |
| 35 | ID1764 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB. |
| | ID1765 | N | DNA TRANSPORT MACHINERY. |
| | ID1766 | N | ORF starting with ATG of length 771 |
| | ID1767 | N | HYPOTHETICAL PROTEIN BH0553. |
| | ID1768 | N | FLAGELLAR HOOK-ASSOCIATED PROTEIN 3 (HAP3). |
| 40 | ID1769 | N | ORF starting with ATG of length 762 |
| | ID1770 | N | FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (FLGK). |
| | ID1771 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPA. |
| | ID1772 | N | FLAGELLAR BIOSYNTHESIS PROTEIN FLHF (FLAGELLA |
| | ASSOCIATED GTP | | |
| 45 | ID1773 | N | CHEMOTAXIS MOTB PROTEIN (MOTILITY PROTEIN B). |
| | ID1774 | N | FLAGELLAR MOTOR SWITCH PROTEIN. |
| | ID1775 | N | PROTEIN-EXPORT MEMBRANE PROTEIN. |
| | ID1776 | N | PROTEIN-EXPORT MEMBRANE PROTEIN. |
| | ID1777 | N | ORF starting with ATG of length 522 |
| 50 | ID1778 | N | PREPROTEIN TRANSLOCASE SUBUNIT. |
| | ID1779 | N | FLAGELLAR-SPECIFIC ATP SYNTHASE. |
| | ID1780 | N | FLAGELLAR MOTOR SWITCH PROTEIN. |
| | ID1781 | N | ORF starting with ATG of length 763 |
| | ID1782 | N | BH0721 PROTEIN. |
| 55 | ID1783 | N | PREPROTEIN TRANSLOCASE SECY SUBUNIT. |
| | ID1784 | N | ORF starting with ATG of length 2031 |
| | ID1785 | N | SIGNAL PEPTIDASE (TYPE I). |
| | ID1786 | N | PREPROTEIN TRANSLOCASE SECY SUBUNIT. |
| | ID1787 | N | FLAGELLAR BASAL-BODY M-RING PROTEIN. |
| 60 | ID1788 | N | ORF starting with ATG of length 669 |
| | ID1789 | N | CHEMOTAXIS PROTEIN CHEW. |
| | ID1790 | N | YDII (BH0552 PROTEIN). |
| | ID1791 | N | PREPROTEIN TRANSLOCASE SECA SUBUNIT (FRAGMENT). |
| | ID1792 | N | FLAGELLAR BIOSYNTHETIC PROTEIN FLIP. |
| | ID1793 | N | GTP-BINDING PROTEIN (ELONGATION FACTOR FAMILY). |
| 65 | ID1794 | N | FLAGELLAR HOOK-BASAL BODY PROTEIN. |

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| | ID1795 | N | GTP-BINDING PROTEIN TYPa/BIPA (TYROSINE PHOSPHORYLATED PROTE |
| | ID1796 | N | HYPOTHETICAL 24.1 KDA PROTEIN IN SULA-HELD INTERGENIC REGION |
| 5 | ID1797 | N | SPOIIJ PROTEIN (ESSENTIAL FOR SIGMA-G ACTIVITY AT STAGE III |
| | ID1798 | N | FLAGELLAR HOOK-BASAL BODY PROTEIN. |
| | ID1799 | N | FLAGELLAR HOOK-BASAL BODY COMPLEX PROTEIN FLHO. |
| | ID1800 | N | FLAGELLAR PROTEIN REQUIRED FOR FLAGELLAR FORMATION. |
| 10 | ID1801 | N | FLAGELLAR PROTEIN REQUIRED FOR FLAGELLAR FORMATION. |
| | ID1802 | N | FLAGELLA-ASSOCIATED PROTEIN. |
| | ID1803 | N | FLAGELLAR BIOSYNTHESIS PROTEIN FLHA. |
| | ID1804 | N | METHYL-ACCEPTING CHEMOTAXIS PROTEIN. |
| 15 | ID1805 | N | FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1). |
| | ID1806 | N | TYPE 4 PREPILIN-LIKE PROTEINS LEADER PEPTIDE PROCESSING ENZY |
| | ID1807 | N | SIGNAL PEPTIDASE I (EC 3.4.21.89) (SPASE I) (LEADER PEPTIDAS |
| 20 | ID1808 | N | ORF starting with ATG of length 402 |
| | ID1809 | N | ORF starting with ATG of length 288 |
| | ID1810 | NO | PUTATIVE PROTEASE. |
| | ID1811 | NO | ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT. |
| | ID1812 | NO | ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (EC 3.4.21.). |
| 25 | ID1813 | NT | FLAGELLAR MOTOR SWITCH PROTEIN. |
| | ID1814 | NT | FLAGELLAR MOTOR SWITCH PROTEIN FLIY. |
| | ID1815 | NT | CHEMOTAXIS PROTEIN CHED. |
| | ID1816 | OC | BH1942 PROTEIN. |
| | ID1817 | OC | BH2664 PROTEIN. |
| 30 | ID1818 | O | MINOR EXTRACELLULAR SERINE PROTEASE. |
| | ID1819 | O | PROTEIN-DISULFIDE OXIDOREDUCTASE. |
| | ID1820 | O | TRANSCRIPTIONAL REGULATOR. |
| | ID1821 | O | LEMB (FRAGMENT). |
| | ID1822 | O | PUTATIVE TRANSCRIPTIONAL REGULATOR. |
| 35 | ID1823 | O | YMAD PROTEIN. |
| | ID1824 | O | PYRROLIDONE-CARBOXYLATE PEPTIDASE (EC 3.4.19.3). |
| | ID1825 | O | GLUTATHIONE PEROXIDASE. |
| | ID1826 | O | NITROGEN FIXATION PROTEIN (NIFU PROTEIN). |
| 40 | ID1827 | O | MINOR EXTRACELLULAR SERINE PROTEASE (EC 3.4.21.). |
| | ID1828 | O | ATP-DEPENDENT CLP PROTEASE (HEAT-SHOCK PROTEIN). |
| | ID1829 | O | Subtilisin protein sequence. |
| | ID1830 | O | CLASS III STRESS RESPONSE-RELATED ATPASE. |
| | ID1831 | O | DNA REPAIR PROTEIN. |
| | ID1832 | O | BH3598 PROTEIN. |
| 45 | ID1833 | O | PEPTIDE METHIONINE SULFOXIDE REDUCTASE. |
| | ID1834 | O | BH1447 PROTEIN. |
| | ID1835 | O | CELL-DIVISION PROTEIN (ATP-DEPENDENT ZN METALLOPEPTIDASE) (EC |
| | ID1836 | O | ARGININE UTILIZATION REGULATORY PROTEIN ROCR. |
| 50 | ID1837 | O | THIOREDOXIN REDUCTASE (NADPH) (EC 1.6.4.5). |
| | ID1838 | O | THIOREDOXIN REDUCTASE (EC 1.6.4.5) (TRXR) (GENERAL STRESS PR |
| | ID1839 | O | HEAT-SHOCK PROTEIN (ACTIVATION OF DAK). |
| | ID1840 | O | HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G). |
| 55 | ID1841 | O | ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT (CLASS III HE |
| | ID1842 | O | TRIGGER FACTOR (PROLYL ISOMERASE). |
| | ID1843 | O | ORF starting with ATG of length 612 |
| | ID1844 | O | NEGATIVE EFFECTOR OF THE CONCENTRATION OF HEMA. |
| 60 | ID1845 | O | ARGININE UTILIZATION REGULATORY PROTEIN ROCR. |
| | ID1846 | O | PUTATIVE SIGMA L-DEPENDENT TRANSCRIPTIONAL REGULATOR IN MMGE |
| | ID1847 | O | TRANSCRIPTIONAL REGULATOR (H-T-H). |
| | ID1848 | O | ORF starting with ATG of length 1242 |
| 65 | ID1849 | O | ORF starting with ATG of length 1145 |
| | ID1850 | O | THIOREDOXINE REDUCTASE. |

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| | ID1851 | O | ORF starting with ATG of length 429 |
| | ID1852 | O | 10 KDA CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES). |
| | ID1853 | O | CLASS I HEAT-SHOCK PROTEIN (CHAPERONIN). |
| | ID1854 | O | STAGE V SPORULATION PROTEIN K. |
| 5 | ID1855 | O | CLASS I HEAT-SHOCK PROTEIN (CHAPERONIN). |
| | ID1856 | O | DNA REPAIR PROTEIN. |
| | ID1857 | O | STAGE V SPORULATION PROTEIN K. |
| | ID1858 | O | CLASS I HEAT-SHOCK PROTEIN (CHAPERONIN). |
| | ID1859 | O | BH1623 PROTEIN. |
| 10 | ID1860 | O | PROBABLE O-SIALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57) (GL) |
| | ID1861 | O | SERINE PROTEASE DO. |
| | ID1862 | O | SERINE PROTEASE DO. |
| | ID1863 | O | GENERAL STRESS PROTEIN 170 (GSP170). |
| 15 | ID1864 | O | HEAT-SHOCK PROTEIN (ACTIVATION OF DNAK). |
| | ID1865 | O | CLASS I HEAT-SHOCK PROTEIN (CHAPERONIN). |
| | ID1866 | O | GRPE PROTEIN. |
| | ID1867 | O | CLASS III STRESS RESPONSE-RELATED ATPASE. |
| | ID1868 | O | CYTOCHROME C BIOGENESIS. |
| 20 | ID1869 | O | C5A PEPTIDASE PRECURSOR (EC 3.4.21.-) (SCP). |
| | ID1870 | O | ORF starting with ATG of length 1056 |
| | ID1871 | O | PROTEASE. |
| | ID1872 | O | CLASS III STRESS RESPONSE-RELATED ATPASE. |
| | ID1873 | O | BH2189 PROTEIN. |
| 25 | ID1874 | O | CLASS I HEAT-SHOCK PROTEIN (CHAPERONIN). |
| | ID1875 | O | CELL DIVISION CYCLE CDC48 HOMOLOG (YJOB PROTEIN). |
| | ID1876 | O | CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-). |
| | ID1877 | O | THIOREDOXIN REDUCTASE. |
| | ID1878 | O | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B. |
| 30 | ID1879 | O | BH3598 PROTEIN. |
| | ID1880 | O | PROTEIN SECRETION (POST-TRANSLLOCATION CHAPERONIN). |
| | ID1881 | O | YKVL PROTEIN. |
| | ID1882 | O | ATP-DEPENDENT PROTEASE LA (EC 3.4.21.53). |
| | ID1883 | O | ATP-DEPENDENT PROTEINASE LA (EC 3.4.21.). |
| 35 | ID1884 | O | ATP-DEPENDENT PROTEINASE LA 1 (LON) (CLASS III HEAT-SHOCK PR |
| | ID1885 | O | ATP-DEPENDENT PROTEINASE LA (EC 3.4.21.). |
| | ID1886 | O | NEGATIVE EFFECTOR OF THE CONCENTRATION OF HEMA. |
| | ID1887 | O | Subtilisin protein sequence. |
| 40 | ID1888 | O | GLUTATHIONE PEROXIDASE HOMOLOG BSAA. |
| | ID1889 | O | BH3598 PROTEIN. |
| | ID1890 | O | STAGE V SPORULATION PROTEIN K. |
| | ID1891 | O | CLASS III STRESS RESPONSE-RELATED ATPASE. |
| | ID1892 | O | DNA REPAIR PROTEIN. |
| 45 | ID1893 | O | 10 KDA CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES). |
| | ID1894 | O | CLASS I HEAT-SHOCK PROTEIN (CHAPERONIN). |
| | ID1895 | P | SODIUM-DEPENDENT PHOSPHATE TRANSPORTER. |
| | ID1896 | P | SULFATE ADENYLYLTRANSFERASE. |
| | ID1897 | P | BH1407 PROTEIN. |
| 50 | ID1898 | P | BH1407 PROTEIN. |
| | ID1899 | P | SUPEROXIDE DISMUTASE. |
| | ID1900 | P | Partial sequemce of human manganese superoxide dismutase (hM |
| | ID1901 | P | YDFA PROTEIN. |
| 55 | ID1902 | P | HYPOTHETICAL PROTEIN YWRB. |
| | ID1903 | P | YBXA PROTEIN (ABC TRANSPORTER) (ATP-BINDING PROTEIN). |
| | ID1904 | P | ORF2 (NA+/H+ ANTIPORTER). |
| | ID1905 | P | MULTIPLE RESISTANCE AND PH REGULATION RELATED PROTEIN C. |
| 60 | ID1906 | P | YTGA. |
| | ID1907 | P | FIMA. |
| | ID1908 | P | BH2760 PROTEIN. |
| | ID1909 | P | TRANSCRIPTIONAL REGULATOR (FUR FAMILY). |
| | ID1910 | P | HYPOTHETICAL 31.8 KDA PROTEIN IN GABP-GUAA INTERGENIC REGION |

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| | ID1911 | P | MULTIPLE RESISTANCE AND PH REGULATION RELATED PROTEIN F. |
| | ID1912 | P | MULTIPLE RESISTANCE AND PH REGULATION RELATED PROTEIN E. |
| 5 | ID1913 | P | HYPOTHETICAL 43.2 KDA PROTEIN IN DNAC-RPLI INTERGENIC REGION |
| | ID1914 | P | YVRC PROTEIN. |
| | ID1915 | P | TRANSCRIPTIONAL REGULATOR (FUR FAMILY) (YGAG). |
| | ID1916 | P | YTGD. |
| 10 | ID1917 | P | HYPOTHETICAL 11.3 KDA PROTEIN IN HMP-PROB INTERGENIC REGION. |
| | ID1918 | P | THIOSULFATE SULFURTRANSFERASE. |
| | ID1919 | P | CATALASE X (EC 1.11.1.6). |
| 15 | ID1920 | P | CATION-TRANSPORTING ATPASE (EC 3.6.1.). |
| | ID1921 | P | YVGQ (FRAGMENT). |
| | ID1922 | P | PROBABLE PERMEASE OF ABC TRANSPORTER. |
| | ID1923 | P | PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1.-) (CADMIUM E) |
| 20 | ID1924 | P | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID1925 | P | MGTE. |
| | ID1926 | P | Bacillus megaterium YkoY protein. |
| | ID1927 | P | SA0168 PROTEIN. |
| | ID1928 | P | HYPOTHETICAL 12.2 KDA PROTEIN. |
| | ID1929 | P | SA0579 PROTEIN. |
| 25 | ID1930 | P | HYPOTHETICAL 17.1 KDA PROTEIN IN PHOB-GROES INTERGENIC REGION |
| | ID1931 | P | SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA. |
| | ID1932 | P | Staphylococcus carnosus nitrate reductase NarH subunit. |
| 30 | ID1933 | P | PROBABLE CATION-TRANSPORTING ATPASE F (EC 3.6.1.-). |
| | ID1934 | P | YVGQ PROTEIN. |
| | ID1935 | P | SA0167 PROTEIN. |
| | ID1936 | P | CATION-TRANSPORTING ATPASE PMA1 (EC 3.6.1.-). |
| | ID1937 | P | HYPOTHETICAL 38.5 KDA PROTEIN (FRAGMENT). |
| 35 | ID1938 | P | HYPOTHETICAL 38.5 KDA PROTEIN (FRAGMENT). |
| | ID1939 | P | ARSENICAL PUMP MEMBRANE PROTEIN. |
| | ID1940 | P | YVGP PROTEIN. |
| | ID1941 | P | PUTATIVE ALIPHATIC SULFONATES TRANSPORT ATP-BINDING PROTEIN |
| 40 | ID1942 | P | CADMIUM-TRANSPORTING ATPASE. |
| | ID1943 | P | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID1944 | P | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGI. |
| | ID1945 | P | ORF starting with ATG of length 822 |
| | ID1946 | P | PUTATIVE TRANSCRIPTION REGULATOR. |
| 45 | ID1947 | P | YTLE. |
| | ID1948 | P | PUTATIVE TRANSPORTER. |
| | ID1949 | P | CATALASE X (EC 1.11.1.6). |
| | ID1950 | P | BH2760 PROTEIN. |
| | ID1951 | P | CATALASE. |
| 50 | ID1952 | P | BH1028 PROTEIN. |
| | ID1953 | P | SA1709 PROTEIN. |
| | ID1954 | P | AMMONIUM TRANSPORTER. |
| | ID1955 | P | ALKALINE PHOSPHATASE. |
| | ID1956 | P | PUTATIVE MONOOXYGENASE CY21B4.10C (EC 1.14.13.-). |
| 55 | ID1957 | P | NOVC. |
| | ID1958 | P | STEROID MONOOXYGENASE. |
| | ID1959 | P | PUTATIVE TRANSPORTER. |
| | ID1960 | P | YTLD. |
| 60 | ID1961 | P | ABC TRANSPORTER (PERMEASE). |
| | ID1962 | P | ABC TRANSPORTER (SUBSTRATE-BINDING PROTEIN). |
| | ID1963 | P | HYPOTHETICAL 43.2 KDA PROTEIN IN DNAC-RPLI INTERGENIC REGION |
| | ID1964 | P | ZINC ABC TRANSPORTER PERMEASE PROTEIN. |
| | ID1965 | P | YCEA. |
| 65 | ID1966 | P | ZINC ABC TRANSPORTER ATP BINDING PROTEIN. |

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| | ID1967 | P | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YQGK. |
| | ID1968 | P | YVGP PROTEIN. |
| | ID1969 | P | STEROID MONOOXYGENASE. |
| 5 | ID1970 | P | COPPER-TRANSPORTING ATPASE. |
| | ID1971 | P | SULFATE ABC TRANSPORTER, PERMEASE PROTEIN. |
| | ID1972 | P | POTASSIUM UPTAKE PROTEIN. |
| | ID1973 | P | ORF starting with ATG of length 1164 |
| | ID1974 | P | PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1.-) |
| 10 | (CADMIUM E | | |
| | ID1975 | P | COPPER-TRANSPORTING ATPASE. |
| | ID1976 | P | SULFATE ABC TRANSPORTER (PERMEASE). |
| | ID1977 | P | PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1.-) |
| | (CADMIUM E | | |
| 15 | ID1978 | P | BH1440 PROTEIN. |
| | ID1979 | P | CHROMATE TRANSPORTER. |
| | ID1980 | P | SULFATE ADENYLYLTRANSFERASE (EC 2.7.7.4) (SULFATE |
| | ADENYLATET | | |
| | ID1981 | P | CHROMATE TRANSPORTER. |
| 20 | ID1982 | P | NA+/H+ ANTIPORTER. |
| | ID1983 | P | HYPOTHETICAL 28.4 KDA PROTEIN IN SACT-SACP INTERGENIC |
| | REGION | | |
| | ID1984 | P | SA0582 PROTEIN. |
| | ID1985 | P | PROBABLE CATION-TRANSPORTING ATPASE F (EC 3.6.1.-). |
| 25 | ID1986 | P | CATION-TRANSPORTING P-ATPASE PACL. |
| | ID1987 | P | CATALASE (EC 1.11.1.6). |
| | ID1988 | P | CATALASE (EC 1.11.1.6). |
| | ID1989 | P | YTGC. |
| | ID1990 | P | ORF starting with ATG of length 470 |
| 30 | ID1991 | P | SUPEROXIDE DISMUTASE. |
| | ID1992 | P | ABC TRANSPORTER ATP-BINDING SUBUNIT. |
| | ID1993 | P | CHAPERONIN. |
| | ID1994 | P | HYPOTHETICAL 57.2 KDA PROTEIN. |
| | ID1995 | P | BH2861 PROTEIN. |
| 35 | ID1996 | P | PUTATIVE ABC-TRANSPORTER (FRAGMENT). |
| | ID1997 | P | NITRITE EXTRUSION PROTEIN (NITRITE FACILITATOR). |
| | ID1998 | P | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGH. |
| | ID1999 | P | NA+-TRANSPORTING ATP SYNTHASE. |
| | ID2000 | P | YVGR PROTEIN. |
| 40 | ID2001 | P | CARBONIC ANHYDRASE. |
| | ID2002 | P | PHOSPHONATES TRANSPORT SYSTEM (PERMEASE). |
| | ID2003 | P | NA+-TRANSPORTING ATP SYNTHASE. |
| | ID2004 | P | SUPEROXIDE DISMUTASE. |
| | ID2005 | P | YVGR PROTEIN. |
| 45 | ID2006 | P | ABC TRANSPORTER ATP-BINDING SUBUNIT. |
| | ID2007 | P | CADMIUM-TRANSPORTING ATPASE. |
| | ID2008 | P | NITRITE EXTRUSION PROTEIN (NITRITE FACILITATOR). |
| | ID2009 | P | FERRITIN. |
| | ID2010 | P | STEROID MONOOXYGENASE. |
| 50 | ID2011 | P | ORF starting with ATG of length 723 |
| | ID2012 | P | YCEA. |
| | ID2013 | PH | Corynebacterium glutamicum MCT protein SEQ ID NO:566. |
| | ID2014 | PH | YVRB PROTEIN. |
| | ID2015 | PH | ORF starting with ATG of length 567 |
| 55 | ID2016 | PH | HOMOLOGUE OF FERRIC ANGUIBACTIN TRANSPORT SYSTEM |
| | PERMEASE P | | |
| | ID2017 | PH | ORF starting with ATG of length 954 |
| | ID2018 | PH | HOMOLOGUE OF FERRIC ANGUIBACTIN TRANSPORT SYSTEM |
| | PERMEASE P | | |
| 60 | ID2019 | PH | HOMOLOGUE OF IRON DICITRATE TRANSPORT ATP-BINDING |
| | PROTEIN FE | | |
| | ID2020 | PH | FERRICHROME ABC TRANSPORTER (PERMEASE). |
| | ID2021 | PH | FERRICHROME TRANSPORT ATP-BINDING PROTEIN FHUC. |
| | ID2022 | PH | FERRICHROME TRANSPORT SYSTEM PERMEASE PROTEIN FHUG. |
| 65 | ID2023 | PR | ASSIMILATORY NITRITE REDUCTASE (SUBUNIT). |
| | ID2024 | PR | ASSIMILATORY NITRITE REDUCTASE (SUBUNIT). |

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| | ID2025 | PR | ASSIMILATORY NITRITE REDUCTASE (SUBUNIT). |
| | ID2026 | Q | YERP PROTEIN. |
| | ID2027 | Q | ORF starting with ATG of length 929 |
| | ID2028 | Q | BH2163 PROTEIN. |
| 5 | ID2029 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2030 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2031 | Q | SPORE COAT PROTEIN A. |
| | ID2032 | Q | NATA. |
| | ID2033 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 10 | ID2034 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2035 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2036 | Q | BH3008 PROTEIN. |
| | ID2037 | Q | IMIDAZOLEPROPIONASE (EC 3.5.2.7) (IMIDAZOLE-5- |
| | PROPIONATE | | |
| 15 | ID2038 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2039 | Q | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN |
| | ACDA 5'R | | |
| | ID2040 | Q | BH1071 PROTEIN. |
| | ID2041 | Q | SPAF. |
| 20 | ID2042 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2043 | Q | NARINGENIN-CHALCONE SYNTHASE. |
| | ID2044 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2045 | Q | HYPOTHETICAL 20.8 KDA PROTEIN IN SERS-DNAZ INTERGENIC |
| | REGION | | |
| 25 | ID2046 | Q | SA0829 PROTEIN. |
| | ID2047 | Q | BH3008 PROTEIN. |
| | ID2048 | Q | Amino acid sequence of picromycin/methymycin |
| | cytochrome P450 | | |
| | ID2049 | Q | BH3008 PROTEIN. |
| 30 | ID2050 | Q | DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (NEURAL |
| | SPECIF | | |
| | ID2051 | Q | ORF starting with ATG of length 669 |
| | ID2052 | Q | ABC TRANSPORTER ATP-BINDING PROTEIN. |
| | ID2053 | Q | ACETYLXYLAN ESTERASE (CEPHALOSPORIN-C DEACETYLASE) |
| 35 | (EC 3.1.1 | | |
| | ID2054 | Q | YERP PROTEIN. |
| | ID2055 | Q | PUTATIVE TRANSMEMBRANE PROTEIN (FRAGMENT). |
| | ID2056 | Q | HYPOTHETICAL 28.2 KDA PROTEIN. |
| | ID2057 | Q | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN |
| 40 | GLVBC | | |
| | ID2058 | Q | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN |
| | GLVBC | | |
| | ID2059 | Q | HYPOTHETICAL 64.5 KDA PROTEIN. |
| | ID2060 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 45 | ID2061 | Q | ABC TRANSPORTER ATP-BINDING PROTEIN. |
| | ID2062 | Q | YERP PROTEIN. |
| | ID2063 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2064 | Q | ORF starting with ATG of length 639 |
| | ID2065 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 50 | ID2066 | Q | ORF starting with ATG of length 951 |
| | ID2067 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2068 | Q | Group B Streptococcus protein sequence SEQ ID NO:4. |
| | ID2069 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2070 | Q | 4-HYDROXYPHENYLACETATE-3-HYDROXYLASE. |
| 55 | ID2071 | Q | FATTY ACID ALPHA HYDROXYLASE. |
| | ID2072 | Q | SA1734 PROTEIN. |
| | ID2073 | Q | BH2620 PROTEIN. |
| | ID2074 | Q | MRSF PROTEIN. |
| | ID2075 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 60 | ID2076 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2077 | Q | YERP PROTEIN. |
| | ID2078 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2079 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2080 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 65 | ID2081 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2082 | Q | BH2163 PROTEIN. |

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| | ID2083 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2084 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2085 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 5 | ID2086 | Q | ORF starting with ATG of length 461 |
| | ID2087 | Q | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2088 | QR | BH3955 PROTEIN. |
| | ID2089 | QR | Amino acid sequence of a beta-ketoacyl-ACP reductase |
| | protein | | |
| 10 | ID2090 | QR | 3-OXOACYL- [ACYL-CARRIER PROTEIN] REDUCTASE (EC |
| | 1.1.1.100) | (3 | |
| | ID2091 | QR | 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL |
| | DEHYDROGENASE. | | |
| | ID2092 | QR | D-MANNONATE OXIDOREDUCTASE. |
| 15 | ID2093 | QR | BH2367 PROTEIN. |
| | ID2094 | QR | YVAG PROTEIN. |
| | ID2095 | QR | SORBITOL-6-PHOSPHATE DEHYDROGENASE. |
| | ID2096 | QR | ORF starting with ATG of length 810 |
| | ID2097 | QR | 3-OXOACYL- [ACYL-CARRIER PROTEIN] REDUCTASE. |
| 20 | ID2098 | QR | ORF starting with ATG of length 885 |
| | ID2099 | QR | DEHYDROGENASE/REDUCTASE FAMILY. |
| | ID2100 | QR | 2-DEOXY-D-GLUCONATE 3-DEHYDROGENASE (EC 1.1.1.125). |
| | ID2101 | QR | HYPOTHETICAL OXIDOREDUCTASE IN RTP-PELB INTERGENIC |
| | REGION (E | | |
| 25 | ID2102 | QR | BH1330 PROTEIN. |
| | ID2103 | QR | BH0410 PROTEIN. |
| | ID2104 | QR | 3-OXOACYL- [ACYL CARRIER PROTEIN] REDUCTASE. |
| | ID2105 | QR | SHORT CHAIN ALCOHOL DEHYDROGENASE. |
| | ID2106 | QR | HYPOTHETICAL 28.3 KDA PROTEIN IN XPAC-ABRB INTERGENIC |
| 30 | REGION | | |
| | ID2107 | QR | HYPOTHETICAL OXIDOREDUCTASE IN CHEV-MOBA INTERGENIC |
| | REGION (E | | |
| | ID2108 | QR | ORF starting with ATG of length 504 |
| | ID2109 | QR | D-MANNONATE OXIDOREDUCTASE. |
| 35 | ID2110 | QR | 3-OXOACYL- (ACYL-CARRIER PROTEIN) REDUCTASE (EC |
| | 1.1.1.100) | . | |
| | ID2111 | QR | 3-OXOACYL- [ACYL CARRIER PROTEIN] REDUCTASE. |
| | ID2112 | R | INDOLE-3-ACETYL-ASPARTIC ACID HYDROLASE. |
| | ID2113 | R | BH3467 PROTEIN. |
| 40 | ID2114 | R | HYPOTHETICAL 13.6 KDA PROTEIN. |
| | ID2115 | R | HMRA. |
| | ID2116 | R | HYPOTHETICAL 30.2 KDA PROTEIN IN IDH-DEOR INTERGENIC |
| | REGION. | | |
| | ID2117 | R | HYPOTHETICAL 38.3 KDA PROTEIN. |
| | ID2118 | R | METHANOL DEHYDROGENASE REGULATORY PROTEIN. |
| 45 | ID2119 | R | PUTATIVE ABC TRANSPORTER, INTEGRAL MEMBRANE SUBUNIT. |
| | ID2120 | R | HYPOTHETICAL PROTEIN. |
| | ID2121 | R | IMMUNOGENIC PROTEIN. |
| | ID2122 | R | YBFQ PROTEIN. |
| 50 | ID2123 | R | BH2689 PROTEIN. |
| | ID2124 | R | PUTATIVE ESTERASE/LIPASE. |
| | ID2125 | R | BH1482 PROTEIN. |
| | ID2126 | R | BH1746 PROTEIN. |
| | ID2127 | R | YKPA PROTEIN. |
| | ID2128 | R | SPORE CORTEX PROTEIN. |
| 55 | ID2129 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2130 | R | CARBOXYLESTERASE. |
| | ID2131 | R | GUAB (FRAGMENT). |
| | ID2132 | R | YLQF (BH2476 PROTEIN). |
| 60 | ID2133 | R | BH1362 PROTEIN. |
| | ID2134 | R | SODIUM-DEPENDENT TRANSPORTER. |
| | ID2135 | R | SEQUENCE 1 FROM PATENT WO9934002. |
| | ID2136 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2137 | R | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2138 | R | BH3108 PROTEIN. |
| 65 | ID2139 | R | HMRA. |

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| | ID2140 | R | LATE COMPETENCE OPERON REQUIRED FOR DNA BINDING AND |
| | UPTAKE. | | |
| | ID2141 | R | BH2099 PROTEIN. |
| 5 | ID2142 | R | ORF starting with ATG of length 734 |
| | ID2143 | R | PHENOL 2-HYDROXYLASE COMPONENT B. |
| | ID2144 | R | BH2155 PROTEIN. |
| | ID2145 | R | ATP-BINDING PROTEIN. |
| | ID2146 | R | HYPOTHETICAL PROTEIN PA4923. |
| 10 | ID2147 | R | BH1122 PROTEIN. |
| | ID2148 | R | BH1372 PROTEIN. |
| | ID2149 | R | BH3923 PROTEIN. |
| | ID2150 | R | ORF starting with ATG of length 599 |
| | ID2151 | R | BH3254 PROTEIN. |
| 15 | ID2152 | R | B. subtilis hydrolase protein YFHM. |
| | ID2153 | R | BH0079 PROTEIN. |
| | ID2154 | R | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2155 | R | BH1308 PROTEIN. |
| | ID2156 | R | YKOQ. |
| 20 | ID2157 | R | YISU PROTEIN. |
| | ID2158 | R | BH3866 PROTEIN. |
| | ID2159 | R | HYPOTHETICAL 37.5 KDA PROTEIN IN DEGA-NPRB INTERGENIC |
| | REGION | | |
| | ID2160 | R | ORF starting with ATG of length 570 |
| 25 | ID2161 | R | RIBOSOMAL-PROTEIN (S18)-ALANINE ACETYLTRANSFERASE. |
| | ID2162 | R | BH1956 PROTEIN. |
| | ID2163 | R | HYPOTHETICAL 32.8 KDA PROTEIN. |
| | ID2164 | R | HYPOTHETICAL 17.9 KDA PROTEIN IN PHOB-GROES |
| | INTERGENIC REGIO | | |
| 30 | ID2165 | R | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2166 | R | BH3279 PROTEIN. |
| | ID2167 | R | PHT4-RELATED PROTEIN. |
| | ID2168 | R | BH0392 PROTEIN. |
| | ID2169 | R | BH1700 PROTEIN. |
| 35 | ID2170 | R | ORF starting with ATG of length 933 |
| | ID2171 | R | NADH OXIDASE (EC 1.6.99.3) (NOXASE). |
| | ID2172 | R | Neisseria meningitidis strain A antigen encoded by |
| | ORF6. | | |
| | ID2173 | R | MMGE PROTEIN. |
| 40 | ID2174 | R | HYPOTHETICAL 23.3 KDA PROTEIN. |
| | ID2175 | R | PENICILLIN G ACYLASE. |
| | ID2176 | R | PROTEASE (PROCESSING OF PRO-SIGMA-K TO ACTIVE SIGMA- |
| | K). | | |
| | ID2177 | R | BH3470 PROTEIN. |
| | ID2178 | R | BH2835 PROTEIN. |
| 45 | ID2179 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN |
| | TM0352. | | |
| | ID2180 | R | SODIUM-DEPENDENT TRANSPORTER. |
| | ID2181 | R | HYPOTHETICAL 37.8 KDA PROTEIN. |
| | ID2182 | R | BH2854 PROTEIN. |
| 50 | ID2183 | R | MLL8760 PROTEIN. |
| | ID2184 | R | HYPOTHETICAL 28.1 KDA PROTEIN IN SIPU 3'REGION. |
| | ID2185 | R | ORF starting with ATG of length 600 |
| | ID2186 | R | HYPOTHETICAL 32.2 KDA PROTEIN. |
| | ID2187 | R | PUTATIVE OXIDOREDUCTASE. |
| 55 | ID2188 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2189 | R | BH3572 PROTEIN. |
| | ID2190 | R | ABC TRANSPORTER. |
| | ID2191 | R | ABC TRANSPORTER. |
| 60 | ID2192 | R | BH3569 PROTEIN. |
| | ID2193 | R | YUSC PROTEIN. |
| | ID2194 | R | ORF starting with ATG of length 621 |
| | ID2195 | R | BH1266 PROTEIN. |
| | ID2196 | R | BH1896 PROTEIN. |
| 65 | ID2197 | R | SA0211 PROTEIN. |
| | ID2198 | R | BH1421 PROTEIN. |
| | ID2199 | R | ABC TRANSPORTER, PERMEASE PROTEIN. |

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| | ID2200 | R | BH2013 PROTEIN. |
| | ID2201 | R | ORF starting with ATG of length 701 |
| | ID2202 | R | BH2498 PROTEIN. |
| 5 | ID2203 | R | ORF starting with ATG of length 474 |
| | ID2204 | R | THERMOSTABLE CARBOXYPEPTIDASE (CPSA-2) (EC 3.4.17.). |
| | ID2205 | R | ORF starting with ATG of length 972 |
| | ID2206 | R | ORF starting with ATG of length 396 |
| | ID2207 | R | CARBOXYLESTERASE. |
| 10 | ID2208 | R | ORF starting with ATG of length 431 |
| | ID2209 | R | METHANOL DEHYDROGENASE REGULATORY PROTEIN. |
| | ID2210 | R | BH0720 PROTEIN. |
| | ID2211 | R | COMPETENCE-DAMAGE INDUCIBLE PROTEIN CINA. |
| | ID2212 | R | HYPOTHETICAL 36.8 KDA PROTEIN. |
| 15 | ID2213 | R | BH3279 PROTEIN. |
| | ID2214 | R | Bacillus subtilis metalloprotease YhaA. |
| | ID2215 | R | SPORE CORTEX PROTEIN. |
| | ID2216 | R | BH0287 PROTEIN. |
| | ID2217 | R | BH0287 PROTEIN. |
| 20 | ID2218 | R | HYPOTHETICAL 43.5 KDA PROTEIN. |
| | ID2219 | R | WZX. |
| | ID2220 | R | AMINOBENZOYL-GLUTAMATE UTILIZATION PROTEIN A HOMOLOG. |
| | ID2221 | R | BH2392 PROTEIN. |
| | ID2222 | R | HYPOTHETICAL 49.4 KDA PROTEIN. |
| 25 | ID2223 | R | BH2703 PROTEIN. |
| | ID2224 | R | FLORFENICOL RESISTANCE PROTEIN. |
| | ID2225 | R | BH0105 PROTEIN. |
| | ID2226 | R | BH2921 PROTEIN. |
| | ID2227 | R | HYPOTHETICAL. |
| 30 | ID2228 | R | BH2279 PROTEIN. |
| | ID2229 | R | ORF starting with ATG of length 552 |
| | ID2230 | R | BH4031 PROTEIN. |
| | ID2231 | R | HYPOTHETICAL PROTEIN. |
| | ID2232 | R | BH3883 PROTEIN. |
| 35 | ID2233 | R | BH1700 PROTEIN. |
| | ID2234 | R | BH0531 PROTEIN. |
| | ID2235 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2236 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2237 | R | ORF starting with ATG of length 626 |
| | ID2238 | R | BH0822 PROTEIN. |
| 40 | ID2239 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN |
| | YDIF. | | |
| | ID2240 | R | BH0560 PROTEIN. |
| | ID2241 | R | NADH OXIDASE (NOX). |
| | ID2242 | R | YLQF (BH2476 PROTEIN). |
| 45 | ID2243 | R | HYPOTHETICAL PROTEIN YWRF. |
| | ID2244 | R | BH2835 PROTEIN. |
| | ID2245 | R | ORF starting with ATG of length 489 |
| | ID2246 | R | SA0780 PROTEIN. |
| | ID2247 | R | HYPOTHETICAL 19.2 KDA PROTEIN IN RPH-ILVB INTERGENIC |
| 50 | REGION. | | |
| | ID2248 | R | BH2805 PROTEIN. |
| | ID2249 | R | ORF starting with ATG of length 906 |
| | ID2250 | R | NADH-DEPENDENT DEHYDROGENASE HOMOLOG. |
| | ID2251 | R | LATE COMPETENCE OPERON REQUIRED FOR DNA BINDING AND |
| 55 | UPTAKE. | | |
| | ID2252 | R | HYPOTHETICAL PROTEIN. |
| | ID2253 | R | ABC TRANSPORTER ATP BINDING PROTEIN. |
| | ID2254 | R | ORFL1. |
| | ID2255 | R | HYPOTHETICAL 73.4 KDA PROTEIN. |
| 60 | ID2256 | R | HYPOTHETICAL 44.4 KDA PROTEIN IN EPR-GALK INTERGENIC |
| | REGION. | | |
| | ID2257 | R | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2258 | R | ORF starting with ATG of length 663 |
| | ID2259 | R | BH1362 PROTEIN. |
| 65 | ID2260 | R | PUTATIVE TRANSPORTER. |
| | ID2261 | R | RIBONUCLEASE H-RELATED PROTEIN. |

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| | ID2262 | R | BH2393 PROTEIN. |
| | ID2263 | R | INVOLVED IN SPORE CORTEX SYNTHESIS. |
| | ID2264 | R | BH1363 PROTEIN. |
| | ID2265 | R | BH1362 PROTEIN. |
| 5 | ID2266 | R | GTP-BINDING PROTEIN INVOLVED IN INITIATION OF SPORULATION. |
| | ID2267 | R | BH0106 PROTEIN. |
| | ID2268 | R | YTPR. |
| | ID2269 | R | BH0052 PROTEIN. |
| 10 | ID2270 | R | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID2271 | R | BH1746 PROTEIN. |
| | ID2272 | R | BH1089 PROTEIN. |
| | ID2273 | R | <i>Bacillus subtilis</i> metalloprotease YmfH. |
| | ID2274 | R | THDF PROTEIN (THIOPHEN AND FURAN OXIDATION). |
| 15 | ID2275 | R | BH0487 PROTEIN. |
| | ID2276 | R | BH2820 PROTEIN. |
| | ID2277 | R | BH3178 PROTEIN. |
| | ID2278 | R | TRANSCRIPTIONAL REGULATOR INVOLVED IN NITROGEN REGULATION (N). |
| 20 | ID2279 | R | YFIN (BH1056 PROTEIN). |
| | ID2280 | R | BH3470 PROTEIN. |
| | ID2281 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2282 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA. |
| 25 | ID2283 | R | HYPOTHETICAL 89.7 KDA PROTEIN. |
| | ID2284 | R | HYPOTHETICAL 8.1 KDA PROTEIN IN KDGK 5'REGION (K2 ORF). |
| | ID2285 | R | BH3359 PROTEIN. |
| | ID2286 | R | BH2393 PROTEIN. |
| 30 | ID2287 | R | HYPOTHETICAL 33.7 KDA PROTEIN. |
| | ID2288 | R | BH1669 PROTEIN. |
| | ID2289 | R | PHOSPHOGLYCOLATE PHOSPHATASE. |
| | ID2290 | R | ORF starting with ATG of length 397 |
| | ID2291 | R | BH3054 PROTEIN. |
| 35 | ID2292 | R | HYPOTHETICAL 24.1 KDA PROTEIN YDIH. |
| | ID2293 | R | BH1266 PROTEIN. |
| | ID2294 | R | BH1266 PROTEIN. |
| | ID2295 | R | BH0608 PROTEIN. |
| | ID2296 | R | HYPOTHETICAL 73.4 KDA PROTEIN. |
| 40 | ID2297 | R | HYPOTHETICAL 43.4 KDA PROTEIN IN CTAF 3'REGION (ORF2). |
| | ID2298 | R | BH3254 PROTEIN. |
| | ID2299 | R | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2300 | R | BH2587 PROTEIN. |
| 45 | ID2301 | R | CG3609 PROTEIN. |
| | ID2302 | R | ORF starting with ATG of length 431 |
| | ID2303 | R | BH2165 PROTEIN. |
| | ID2304 | R | Staphylococcal ABC transporter protein. |
| | ID2305 | R | ORF starting with ATG of length 574 |
| 50 | ID2306 | R | GTP-BINDING PROTEIN INVOLVED IN INITIATION OF SPORULATION. |
| | ID2307 | R | BH2503 PROTEIN. |
| | ID2308 | R | HYPOTHETICAL 41.6 KDA PROTEIN IN FMT-SPOVM INTERGENIC REGION. |
| 55 | ID2309 | R | UNKNOWN. |
| | ID2310 | R | COMF OPERON PROTEIN 3. |
| | ID2311 | R | ORF starting with ATG of length 347 |
| | ID2312 | R | BH3121 PROTEIN. |
| | ID2313 | R | BH2498 PROTEIN. |
| 60 | ID2314 | R | BH0720 PROTEIN. |
| | ID2315 | R | COMPETENCE-DAMAGE INDUCIBLE PROTEIN. |
| | ID2316 | R | ORF starting with ATG of length 465 |
| | ID2317 | R | HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN IDH 3'RE. |
| 65 | ID2318 | R | ORF11. |
| | ID2319 | R | IMMUNOGENIC PROTEIN. |

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| | ID2320 | R | BH1271 PROTEIN. |
| | ID2321 | R | GTP-BINDING PROTEIN (ERA/THDF FAMILY). |
| | ID2322 | R | JAG PROTEIN (SPOIIILJ-ASSOCIATED PROTEIN). |
| | ID2323 | R | BH2906 PROTEIN. |
| 5 | ID2324 | R | BH3090 PROTEIN. |
| | ID2325 | R | BH3467 PROTEIN. |
| | ID2326 | R | BH3359 PROTEIN. |
| | ID2327 | R | ORF starting with ATG of length 452 |
| | ID2328 | R | BH3090 PROTEIN. |
| 10 | ID2329 | R | BH2378 PROTEIN. |
| | ID2330 | R | ORFA1. |
| | ID2331 | R | PUTATIVE VIRULENCE FACTOR. |
| | ID2332 | R | BH1811 PROTEIN. |
| 15 | ID2333 | R | YKVM PROTEIN. |
| | ID2334 | R | BH0590 PROTEIN. |
| | ID2335 | R | HYPOTHETICAL 32.8 KDA PROTEIN. |
| | ID2336 | R | HOMOLOGUES TO NITRILE HYDRATASE REGION 3'- HYPOTHETICAL PROTEIN. |
| 20 | ID2337 | R | HYPOTHETICAL 35.7 KDA PROTEIN. |
| | ID2338 | R | ATP-BINDING PROTEIN ABC. |
| | ID2339 | R | ORF starting with ATG of length 549 |
| | ID2340 | R | BH1679 PROTEIN. |
| | ID2341 | R | ORF starting with ATG of length 1227 |
| | ID2342 | R | UNKNOWN (BH3837 PROTEIN). |
| 25 | ID2343 | R | BH2972 PROTEIN. |
| | ID2344 | R | SODIUM-DEPENDENT TRANSPORTER. |
| | ID2345 | R | HYPOTHETICAL 28.1 KDA PROTEIN IN SIPU 3'REGION. |
| | ID2346 | R | BH2030 PROTEIN. |
| 30 | ID2347 | R | MYO-INOSITOL 2-DEHYDROGENASE. |
| | ID2348 | R | BH3289 PROTEIN. |
| | ID2349 | R | Ammonifex degensii KC4 alkaline phosphatase (3A1A=3A2A). |
| | ID2350 | R | ORF starting with ATG of length 756 |
| | ID2351 | R | ALUMINUM RESISTANCE PROTEIN (FRAGMENT). |
| 35 | ID2352 | R | BH1047 PROTEIN. |
| | ID2353 | R | ORF starting with ATG of length 749 |
| | ID2354 | R | FORMATE DEHYDROGENASE ALPHA SUBUNIT HOMOLOG. |
| | ID2355 | R | BH1746 PROTEIN. |
| | ID2356 | R | ORF starting with ATG of length 750 |
| 40 | ID2357 | R | HYPOTHETICAL PROTEIN YWRF. |
| | ID2358 | R | BH1362 PROTEIN. |
| | ID2359 | R | WZX. |
| | ID2360 | R | YMFF PROTEIN. |
| | ID2361 | R | BH2393 PROTEIN. |
| 45 | ID2362 | R | BH2392 PROTEIN. |
| | ID2363 | R | ORF starting with ATG of length 933 |
| | ID2364 | R | ORF starting with ATG of length 1126 |
| | ID2365 | R | BH1421 PROTEIN. |
| | ID2366 | R | HYPOTHETICAL 26.3 KDA PROTEIN. |
| 50 | ID2367 | R | HYPOTHETICAL 36.8 KDA PROTEIN. |
| | ID2368 | R | HYPOTHETICAL 33.7 KDA PROTEIN. |
| | ID2369 | R | BH0105 PROTEIN. |
| | ID2370 | R | BH0106 PROTEIN. |
| | ID2371 | R | BH2921 PROTEIN. |
| 55 | ID2372 | R | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2373 | R | YLQF (BH2476 PROTEIN). |
| | ID2374 | R | HYPOTHETICAL 19.2 KDA PROTEIN IN RPH-ILVB INTERGENIC REGION. |
| | ID2375 | R | PUTATIVE TRANSPORTER. |
| 60 | ID2376 | R | CMP-BINDING PROTEIN. |
| | ID2377 | R | ORF starting with ATG of length 559 |
| | ID2378 | R | ORF starting with ATG of length 216 |
| | ID2379 | R | ORF starting with ATG of length 202 |
| | ID2380 | R | ORF starting with ATG of length 339 |
| 65 | ID2381 | R | ORF starting with ATG of length 386 |
| | ID2382 | S | GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE. |

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| | ID2383 | S | BH2588 PROTEIN. |
| | ID2384 | S | BH1442 PROTEIN. |
| | ID2385 | S | BH1440 PROTEIN. |
| | ID2386 | S | BH1437 PROTEIN. |
| 5 | ID2387 | S | BH1436 PROTEIN. |
| | ID2388 | S | CITS (TWO-COMPONENT SENSOR HISTIDINE KINASE). |
| | ID2389 | S | ORF starting with ATG of length 324 |
| | ID2390 | S | HYPOTHETICAL 16.2 KDA PROTEIN IN COMF-FLGM INTERGENIC |
| | REGION | | |
| 10 | ID2391 | S | PUTATIVE TWO-COMPONENT SYSTEM SENSOR KINASE. |
| | ID2392 | S | DNA, COMPLETE SEQUENCE. |
| | ID2393 | S | GTP-BINDING PROTEIN. |
| | ID2394 | S | BH4052 PROTEIN. |
| 15 | ID2395 | S | BH1263 PROTEIN. |
| | ID2396 | S | BH2161 PROTEIN. |
| | ID2397 | S | ORF starting with ATG of length 315 |
| | ID2398 | S | BH1789 PROTEIN. |
| | ID2399 | S | ORF starting with ATG of length 302 |
| | ID2400 | S | YDHG PROTEIN. |
| 20 | ID2401 | S | MULTIDRUG RESISTANCE PROTEIN. |
| | ID2402 | S | BH1496 PROTEIN. |
| | ID2403 | S | ORF starting with ATG of length 510 |
| | ID2404 | S | DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP |
| | EPIMERASE). | | |
| 25 | ID2405 | S | BH3939 PROTEIN. |
| | ID2406 | S | ORF starting with ATG of length 330 |
| | ID2407 | S | HYPOTHETICAL 11.7 KDA PROTEIN. |
| | ID2408 | S | Staphylococcus aureus protein homologous to |
| | hypothetical pro | | |
| 30 | ID2409 | S | ORF starting with ATG of length 390 |
| | ID2410 | S | BH1410 PROTEIN. |
| | ID2411 | S | ORF starting with ATG of length 450 |
| | ID2412 | S | ORF starting with ATG of length 499 |
| | ID2413 | S | ORF starting with ATG of length 498 |
| 35 | ID2414 | S | STAGE V SPORULATION PROTEIN AF. |
| | ID2415 | S | STAGE V SPORULATION PROTEIN AE. |
| | ID2416 | S | SPORE GERMINATION PROTEIN A3 PRECURSOR. |
| | ID2417 | S | BH2169 PROTEIN. |
| | ID2418 | S | GCPE PROTEIN HOMOLOG. |
| 40 | ID2419 | S | ORF starting with ATG of length 390 |
| | ID2420 | S | HYPOTHETICAL 19.7 KDA PROTEIN. |
| | ID2421 | S | BH1740 PROTEIN. |
| | ID2422 | S | ORF starting with ATG of length 234 |
| | ID2423 | S | HYPOTHETICAL 18.9 KDA PROTEIN IN CYPA-AADK INTERGENIC |
| 45 | REGION | | |
| | ID2424 | S | ORF starting with ATG of length 237 |
| | ID2425 | S | BH0605 PROTEIN. |
| | ID2426 | S | DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN DRRA. |
| | ID2427 | S | GLUCOSIDASE |
| 50 | ID2428 | S | ORF starting with ATG of length 351 |
| | ID2429 | S | ORF starting with ATG of length 747 |
| | ID2430 | S | ORF starting with ATG of length 336 |
| | ID2431 | S | HYPOTHETICAL 7.1 KDA PROTEIN. |
| 55 | ID2432 | S | ORF starting with ATG of length 363 |
| | ID2433 | S | YFHO PROTEIN. |
| | ID2434 | S | ORF starting with ATG of length 258 |
| | ID2435 | S | HYPOTHETICAL 22.4 KDA PROTEIN IN RPMF-FTSL INTERGENIC |
| | REGION | | |
| 60 | ID2436 | S | ORF starting with ATG of length 336 |
| | ID2437 | S | BH2332 PROTEIN. |
| | ID2438 | S | HYPOTHETICAL 93.5 KDA PROTEIN. |
| | ID2439 | S | ORF starting with ATG of length 314 |
| | ID2440 | S | MANGANESE ABC TRANSPORTER ATP BINDING PROTEIN. |
| | ID2441 | S | TRANSPOSAE FOR TRANSPOSON TN554. |
| 65 | ID2442 | S | HYPOTHETICAL 23.7 KDA PROTEIN. |

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| | ID2443 | S | E. coli proliferation associated protein sequence SEQ |
| | ID NO: | | |
| | ID2444 | S | ORF starting with ATG of length 348 |
| | ID2445 | S | ALDOSE 1-EPIMERASE. |
| 5 | ID2446 | S | BH3567 PROTEIN. |
| | ID2447 | S | SCRT. |
| | ID2448 | S | BH0789 PROTEIN. |
| | ID2449 | S | YFHO PROTEIN. |
| | ID2450 | S | Streptococcus pneumoniae polypeptide. |
| 10 | ID2451 | S | BH1373 PROTEIN. |
| | ID2452 | S | NAD-DEPENDENT METHANOL DEHYDROGENASE. |
| | ID2453 | S | BH1064 PROTEIN. |
| | ID2454 | S | SMALL ACID-SOLUBLE SPORE PROTEIN. |
| | ID2455 | S | ORF starting with ATG of length 621 |
| 15 | ID2456 | S | STREPTOCOCCAL HEMAGGLUTININ. |
| | ID2457 | S | ORF starting with ATG of length 1032 |
| | ID2458 | S | M. tuberculosis polypeptide sequence comprising Mtb-81 antigen |
| | ID2459 | S | ORF starting with ATG of length 885 |
| 20 | ID2460 | S | pJH10 gene product - bacterial endotoxin with insecticidal activity |
| | ID2461 | S | Sequence attached to hepatitis B virus (HBV) pre-S(1) sequence |
| | ID2462 | S | CHLORAMPHENICOL ACETYLTRANSFERASE (EC 2.3.1.28). |
| 25 | ID2463 | S | ORF starting with ATG of length 332 |
| | ID2464 | S | ORF starting with ATG of length 422 |
| | ID2465 | S | GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE. |
| | ID2466 | S | BH1694 PROTEIN. |
| | ID2467 | S | ORF, HYPOTHETICAL PROTEIN. |
| 30 | ID2468 | S | IOLB PROTEIN. |
| | ID2469 | S | ORF starting with ATG of length 322 |
| | ID2470 | S | INVOLVED IN SPORE CORTEX SYNTHESIS. |
| | ID2471 | S | BH1398 PROTEIN. |
| 35 | ID2472 | S | Staphylococcus aureus protein homologous to subunit fmdE. |
| | ID2473 | S | Staphylococcus aureus protein homologous to hypothetical protein |
| | ID2474 | S | SURFACE PROTEIN PLS. |
| | ID2475 | S | BH2296 PROTEIN. |
| 40 | ID2476 | S | BH2295 PROTEIN. |
| | ID2477 | S | HYPOTHETICAL 25.5 KDA PROTEIN. |
| | ID2478 | S | ACETOIN DEHYDROGENASE. |
| | ID2479 | S | YFLM PROTEIN. |
| | ID2480 | S | BH3472 PROTEIN. |
| 45 | ID2481 | S | BH3473 PROTEIN. |
| | ID2482 | S | HYPOTHETICAL 25.7 KDA PROTEIN IN BCSA-DEGR INTERGENIC REGION |
| | ID2483 | S | HYPOTHETICAL 15.7 KDA PROTEIN IN SPOIIIIC-CWLA INTERGENIC REG |
| 50 | ID2484 | S | RELATED TO DIMERIC DIHYDRODIOL DEHYDROGENASE. |
| | ID2485 | S | BH0220 PROTEIN. |
| | ID2486 | S | ORF starting with ATG of length 402 |
| | ID2487 | S | DNA TOPOISOMERASE III-LIKE PROTEIN. |
| | ID2488 | S | L-ASPARAGINASE (EC 3.5.1.1) (L-ASPARAGINE |
| 55 | AMIDOHYDROLASE). | | Amino acid sequence of a partial holB polypeptide. |
| | ID2489 | S | CYTOCHROME P450 107B1 (EC 1.14.-.-) (P450CVIIB1). |
| | ID2490 | S | PUTATIVE ISOCHORISMATASE. |
| | ID2491 | S | HYPOTHETICAL 17.8 KDA PROTEIN. |
| 60 | ID2492 | S | ORF starting with ATG of length 693 |
| | ID2493 | S | SPORE PROTEASE (DEGRADATION OF SASPS). |
| | ID2494 | S | BH4053 PROTEIN. |
| | ID2495 | S | ORF starting with ATG of length 324 |
| | ID2496 | S | BIOTIN SYNTHASE, PUTATIVE. |
| 65 | ID2497 | S | INITIATION OF CHROMOSOME REPLICATION. |
| | ID2498 | S | PROBABLE GLUTAMINASE YLAM (EC 3.5.1.2). |
| | ID2499 | S | |

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| | ID2500 | S | PHOH-LIKE PROTEIN. |
| | ID2501 | S | BH1399 PROTEIN. |
| | ID2502 | S | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN IN OPUD- |
| | BIOI INTER | | |
| 5 | ID2503 | S | ORF starting with ATG of length 933 |
| | ID2504 | S | YOBO. |
| | ID2505 | S | PHAGE-LIKE ELEMENT PBSX PROTEIN XKDV. |
| | ID2506 | S | ORF starting with ATG of length 2268 |
| | ID2507 | S | ORF starting with ATG of length 375 |
| 10 | ID2508 | S | SA2422 PROTEIN. |
| | ID2509 | S | YURZ PROTEIN. |
| | ID2510 | S | BH0817 PROTEIN. |
| | ID2511 | S | BH2983 PROTEIN. |
| | ID2512 | S | ORF starting with ATG of length 564 |
| 15 | ID2513 | S | BH1703 PROTEIN. |
| | ID2514 | S | PROPIONYL-COA CARBOXYLASE, ALPHA SUBUNIT, PUTATIVE. |
| | ID2515 | S | ORF starting with ATG of length 503 |
| | ID2516 | S | HYPOTHETICAL PROTEIN. |
| | ID2517 | S | PROLIDASE (XAA-PRO DIPEPTIDASE) (PEPQ-LIKE2) (EC |
| 20 | 3.4.13.9). | | |
| | ID2518 | S | ORF starting with ATG of length 463 |
| | ID2519 | S | ORF starting with ATG of length 347 |
| | ID2520 | S | ORF starting with ATG of length 279 |
| | ID2521 | S | ORF10. |
| 25 | ID2522 | S | FERRICHROME ABC TRANSPORTER (PERMEASE). |
| | ID2523 | S | GLYCINE BETAINE TRANSPORTER BETL. |
| | ID2524 | S | ORF starting with ATG of length 363 |
| | ID2525 | S | BH3219 PROTEIN. |
| | ID2526 | S | SMALL PROTEIN B. |
| 30 | ID2527 | S | ORF starting with ATG of length 373 |
| | ID2528 | S | BH0893 PROTEIN. |
| | ID2529 | S | YTJA. |
| | ID2530 | S | BH0407 PROTEIN. |
| | ID2531 | S | ORF starting with ATG of length 234 |
| 35 | ID2532 | S | C4-DICARBOXYLATE TRANSPORT SYSTEM (PERMEASE LARGE |
| | PROTEIN). | | |
| | ID2533 | S | CHROMOSOME PARTITION PROTEIN SMC. |
| | ID2534 | S | ORF starting with ATG of length 249 |
| | ID2535 | S | TRANSCRIPTIONAL REGULATOR. |
| 40 | ID2536 | S | TRANSPOSASE (07). |
| | ID2537 | S | PTS SYSTEM, GALACTITOL-SPECIFIC ENZYME II, B |
| | COMPONENT (EC 2 | | |
| | ID2538 | S | ORF starting with ATG of length 547 |
| | ID2539 | S | UNSATURATED GLUCURONYL HYDROLASE. |
| 45 | ID2540 | S | THID. |
| | ID2541 | S | HYPOTHETICAL 56.4 KDA PROTEIN IN SODA-COMGA |
| | INTERGENIC REGIO | | |
| | ID2542 | S | Streptococcus pneumoniae encoded polypeptide. |
| | ID2543 | S | HYPOTHETICAL 14.9 KDA PROTEIN. |
| 50 | ID2544 | S | Amino acid sequence of a Chlamydia pneumoniae protein. |
| | ID2545 | S | HYPOTHETICAL PROTEIN TC0114. |
| | ID2546 | S | PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC |
| | COMPONENT | | |
| | ID2547 | S | HYPOTHETICAL 57.5 KDA PROTEIN IN VMA7-RPS25A |
| 55 | INTERGENIC REGI | | |
| | ID2548 | S | BH0193 PROTEIN. |
| | ID2549 | S | SUGAR TRANSPORT SYSTEM (PERMEASE) (BINDING PROTEIN |
| | DEPENDENT | | |
| | ID2550 | S | GLUCOSE 1-DEHYDROGENASE. |
| 60 | ID2551 | S | SMALL ACID-SOLUBLE SPORE PROTEIN (MAJOR GAMMA-TYPE |
| | SASP). | | |
| | ID2552 | S | TRANSCRIPTIONAL REPRESSOR. |
| | ID2553 | S | BH1432 PROTEIN. |
| | ID2554 | S | BH1770 PROTEIN. |
| 65 | ID2555 | S | ORF13. |
| | ID2556 | S | PROBABLE AMINO ACID PERMEASE. |

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| | ID2557 | S | 228AA LONG HYPOTHETICAL HYDANTOIN RACEMASE. |
| | ID2558 | S | HYPOTHETICAL 30.7 KDA PROTEIN. |
| | ID2559 | S | FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.99) |
| 5 | ID2560 | S | BH2577 PROTEIN. |
| | ID2561 | S | BH2576 PROTEIN. |
| | ID2562 | S | BH2208 PROTEIN. |
| | ID2563 | S | ORF starting with ATG of length 433 |
| | ID2564 | S | ORF starting with ATG of length 567 |
| 10 | ID2565 | S | ORF starting with ATG of length 340 |
| | ID2566 | S | ORF starting with ATG of length 230 |
| | ID2567 | S | ORF starting with ATG of length 340 |
| | ID2568 | S | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2569 | S | BH1373 PROTEIN. |
| 15 | ID2570 | S | STAGE III SPORULATION PROTEIN D. |
| | ID2571 | S | ORF starting with ATG of length 924 |
| | ID2572 | S | BH2734 PROTEIN. |
| | ID2573 | S | BH3113 PROTEIN. |
| | ID2574 | S | BH3134 PROTEIN. |
| 20 | ID2575 | S | ORF starting with ATG of length 569 |
| | ID2576 | S | ORF starting with ATG of length 280 |
| | ID2577 | S | CELL WALL HYDROLASE (SPORULATION). |
| | ID2578 | S | HYPOTHETICAL 20.3 KDA PROTEIN IN UNG-ROCA INTERGENIC REGION. |
| 25 | ID2579 | S | BH3828 PROTEIN. |
| | ID2580 | S | BH3829 PROTEIN. |
| | ID2581 | S | BH0790 PROTEIN. |
| | ID2582 | S | BH3416 PROTEIN. |
| | ID2583 | S | BH2326 PROTEIN. |
| 30 | ID2584 | S | ORF starting with ATG of length 381 |
| | ID2585 | S | BH1357 PROTEIN. |
| | ID2586 | S | BH1704 PROTEIN. |
| | ID2587 | S | BH3063 PROTEIN. |
| | ID2588 | S | BH2916 PROTEIN. |
| 35 | ID2589 | S | SUCROSE-6-PHOSPHATE HYDROLASE. |
| | ID2590 | S | YFLK PROTEIN. |
| | ID2591 | S | HYPOTHETICAL 41.2 KDA PROTEIN. |
| | ID2592 | S | 3-OXOACYL- (ACYL-CARRIER PROTEIN) REDUCTASE. |
| | ID2593 | S | HYPOTHETICAL 33.7 KDA PROTEIN. |
| 40 | ID2594 | S | ORF starting with ATG of length 300 |
| | ID2595 | S | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2596 | S | ORF starting with ATG of length 324 |
| | ID2597 | S | PTS SYSTEM, GLUCOSE-SPECIFIC IIBC COMPONENT (EIIBC-GLC) (GLU) |
| 45 | ID2598 | S | YFHO PROTEIN. |
| | ID2599 | S | BH1692 PROTEIN. |
| | ID2600 | S | DEDA FAMILY PROTEIN. |
| | ID2601 | S | ORF starting with ATG of length 258 |
| | ID2602 | S | BH1610 PROTEIN. |
| 50 | ID2603 | S | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2604 | S | ORF starting with ATG of length 351 |
| | ID2605 | S | SPORE GERMINATION PROTEIN A2. |
| | ID2606 | S | SPORE GERMINATION PROTEIN A3 PRECURSOR. |
| | ID2607 | S | HYPOTHETICAL 27.6 KDA PROTEIN IN FNR-NARG INTERGENIC REGION. |
| 55 | ID2608 | S | BH1148 PROTEIN. |
| | ID2609 | S | BH2691 PROTEIN. |
| | ID2610 | S | YVNB. |
| | ID2611 | S | PUTATIVE INNER MEMBRANE PROTEIN. |
| 60 | ID2612 | S | UNDECAPRENOL KINASE (BACITRACIN RESISTANCE PROTEIN). |
| | ID2613 | S | C4-DICARBOXYLATE TRANSPORT SYSTEM (PERMEASE LARGE PROTEIN). |
| | ID2614 | S | THREONINE SYNTHASE (EC 4.2.99.2). |
| | ID2615 | S | SPORE GERMINATION PROTEIN. |
| 65 | ID2616 | S | HYPOTHETICAL 41.2 KDA PROTEIN IN GAPA-RND INTERGENIC REGION. |

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| | ID2617 | S | PUTATIVE DNA BINDING PROTEIN. |
| | ID2618 | S | ADENINE DEAMINASE. |
| | ID2619 | S | BH1400 PROTEIN. |
| | ID2620 | S | BH1399 PROTEIN. |
| 5 | ID2621 | S | HYPOTHETICAL 13.3 KDA PROTEIN IN AROD-COMER |
| | INTERGENIC REGIO | | |
| | ID2622 | S | TRANSCRIPTIONAL PLEIOTROPIC REPRESSOR. |
| | ID2623 | S | TRYPTOPHANYL-TRNA SYNTHETASE. |
| | ID2624 | S | BH2871 PROTEIN. |
| 10 | ID2625 | S | BH2872 PROTEIN. |
| | ID2626 | S | HYPOTHETICAL 21.0 KDA LIPOPROTEIN IN CSPB-GLPP |
| | INTERGENIC RE | | |
| | ID2627 | S | ORF starting with ATG of length 549 |
| | ID2628 | S | BH1162 PROTEIN. |
| 15 | ID2629 | S | SA2180 PROTEIN. |
| | ID2630 | S | YLNF PROTEIN. |
| | ID2631 | S | BH1789 PROTEIN. |
| | ID2632 | S | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID2633 | S | RNA POLYMERASE SIGMA FACTOR (SIGMA54). |
| 20 | ID2634 | S | BH3562 PROTEIN. |
| | ID2635 | S | PRE-NECK APPENDAGE PROTEIN (LATE PROTEIN GP12). |
| | ID2636 | S | BH1560 PROTEIN. |
| | ID2637 | S | LACTOSE TRANSPORT SYSTEM (PERMEASE). |
| | ID2638 | S | CYSTEINYL-TRNA SYNTHETASE (EC 6.1.1.16) (CYSTEINE-- |
| 25 | TRNA LIGA | | |
| | ID2639 | S | SPORE GERMINATION PROTEIN. |
| | ID2640 | S | TRANSCRIPTIONAL REGULATOR. |
| | ID2641 | S | SPAE. |
| | ID2642 | S | ORF starting with ATG of length 396 |
| 30 | ID2643 | S | ENDO-BETA-1,3-GLUCANASE PRECURSOR. |
| | ID2644 | S | SPORE MATURATION PROTEIN. |
| | ID2645 | S | SPORE MATURATION PROTEIN. |
| | ID2646 | S | YOBO. |
| | ID2647 | S | BH0709 PROTEIN. |
| 35 | ID2648 | S | ORF starting with ATG of length 459 |
| | ID2649 | S | SENSOR KINASE. |
| | ID2650 | S | SENSOR REGULATOR. |
| | ID2651 | S | ORF starting with ATG of length 553 |
| | ID2652 | S | BH2838 PROTEIN. |
| 40 | ID2653 | S | PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGI. |
| | ID2654 | S | BH0618 PROTEIN. |
| | ID2655 | S | BH1625 PROTEIN. |
| | ID2656 | S | YFHO PROTEIN. |
| | ID2657 | S | YFHO PROTEIN. |
| 45 | ID2658 | S | ACETOHYDROXY ACID SYNTHASE (EC 4.1.3.18) |
| | (ACETOLACTATE SYNTH | | |
| | ID2659 | S | ORF starting with ATG of length 588 |
| | ID2660 | S | TRANSPOSASE (22). |
| | ID2661 | S | ORF starting with ATG of length 488 |
| 50 | ID2662 | S | ORF starting with ATG of length 327 |
| | ID2663 | S | ORF starting with ATG of length 354 |
| | ID2664 | S | ORF starting with ATG of length 354 |
| | ID2665 | S | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID2666 | S | ORF starting with ATG of length 474 |
| 55 | ID2667 | S | WZX. |
| | ID2668 | S | TRANSCRIPTIONAL ANTITERMINATOR. |
| | ID2669 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC ENZYME IIA |
| | COMPONENT. | | |
| | ID2670 | S | SORBITOL OPERON ACTIVATOR. |
| 60 | ID2671 | S | BH1565 PROTEIN. |
| | ID2672 | S | BH3147 PROTEIN. |
| | ID2673 | S | STAGE V SPORULATION PROTEIN AF. |
| | ID2674 | S | ORF starting with ATG of length 564 |
| | ID2675 | S | PXO1-40. |
| 65 | ID2676 | S | ORF starting with ATG of length 378 |

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| | ID2677 | S | Human ORFX ORF873 polypeptide sequence SEQ ID NO:1746. |
| | ID2678 | S | BH1913 PROTEIN. |
| 5 | ID2679 | S | ORF starting with ATG of length 567 |
| | ID2680 | S | ORF starting with ATG of length 237 |
| | ID2681 | S | ORF starting with ATG of length 567 |
| | ID2682 | S | YDAS PROTEIN. |
| | ID2683 | S | YFMR. |
| 10 | ID2684 | S | CHORISMATE MUTASE (ISOZYMES 1 AND 2). |
| | ID2685 | S | HYPOTHETICAL 42.4 KDA PROTEIN. |
| | ID2686 | S | BH3142 PROTEIN. |
| | ID2687 | S | HYPOTHETICAL 32.8 KDA PROTEIN PH1052. |
| | ID2688 | S | BH0392 PROTEIN. |
| 15 | ID2689 | S | ORF starting with ATG of length 435 |
| | ID2690 | S | MLL6980 PROTEIN. |
| | ID2691 | S | 217AA LONG HYPOTHETICAL AROM PROTEIN. |
| | ID2692 | S | HYPOTHETICAL 34.0 KDA PROTEIN PH1050. |
| | ID2693 | S | Amino acid sequence of threonyl-tRNA synthetase I. |
| 20 | ID2694 | S | BH3142 PROTEIN. |
| | ID2695 | S | Endo-beta-N-acetylglucosaminidase A. |
| | ID2696 | S | BH0854 PROTEIN. |
| | ID2697 | S | SPORULATION PROTEIN. |
| | ID2698 | S | ORF starting with ATG of length 425 |
| 25 | ID2699 | S | HYPOTHETICAL (PUTATIVE). |
| | ID2700 | S | BH1883 PROTEIN. |
| | ID2701 | S | MULTIDRUG RESISTANCE PROTEIN. |
| | ID2702 | S | STAGE V SPORULATION PROTEIN AF. |
| | ID2703 | S | YUEI PROTEIN. |
| 30 | ID2704 | S | ORF starting with ATG of length 510 |
| | ID2705 | S | ORF1 PROTEIN. |
| | ID2706 | S | YUNF PROTEIN. |
| | ID2707 | S | BH2855 PROTEIN. |
| | ID2708 | S | YJBK PROTEIN. |
| | ID2709 | S | ORF 13. |
| 35 | ID2710 | S | OLIGOPEPTIDE ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| | ID2711 | S | BH0971 PROTEIN. |
| | ID2712 | S | BH0971 PROTEIN. |
| | ID2713 | S | UNKNOWN PROTEIN. |
| 40 | ID2714 | S | ORF starting with ATG of length 360 |
| | ID2715 | S | HYPOTHETICAL 30.7 KDA PROTEIN. |
| | ID2716 | S | BH2709 PROTEIN. |
| | ID2717 | S | SPORE GERMINATION PROTEIN GERYA. |
| | ID2718 | S | SPORE GERMINATION PROTEIN. |
| 45 | ID2719 | S | SPORE GERMINATION PROTEIN. |
| | ID2720 | S | S. pneumoniae derived protein #199. |
| | ID2721 | S | GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE. |
| | ID2722 | S | YUNB PROTEIN. |
| | ID2723 | S | YUNB PROTEIN. |
| 50 | ID2724 | S | 5-KETO-4-DEOXYURONATE ISOMERASE. |
| | ID2725 | S | BH1876 PROTEIN. |
| | ID2726 | S | BH2417 PROTEIN. |
| | ID2727 | S | Nitrate reductase alpha chain protein. |
| | ID2728 | S | BH0697 PROTEIN. |
| 55 | ID2729 | S | ORF starting with ATG of length 347 |
| | ID2730 | S | ORF starting with ATG of length 524 |
| | ID2731 | S | TRANSCRIPTIONAL REGULATOR (ARAC/XYLS FAMILY). |
| | ID2732 | S | BH1350 PROTEIN. |
| | ID2733 | S | Staphylococcus aureus histidine kinase polypeptide sequence. |
| 60 | ID2734 | S | DNA POLYMERASE, BACTERIOPHAGE-TYPE. |
| | ID2735 | S | STAGE V SPORULATION PROTEIN AD. |
| | ID2736 | S | STAGE V SPORULATION PROTEIN AC. |
| | ID2737 | S | BH1418 PROTEIN. |
| | ID2738 | S | MOLYBDOPTERIN BIOSYNTHESIS. |
| 65 | ID2739 | S | NADH-DEPENDENT FMN REDUCTASE (EC 1.6.8.1). |
| | ID2740 | S | SA2369 PROTEIN. |

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| | ID2741 | S | BH1387 PROTEIN. |
| | ID2742 | S | BETA-GLUCOSIDASE. |
| | ID2743 | S | ORF starting with ATG of length 540 |
| | ID2744 | S | ASSIMILATORY NITRATE REDUCTASE ELECTRON TRANSFER |
| 5 | SUBUNIT. | | |
| | ID2745 | S | BH1114 PROTEIN. |
| | ID2746 | S | ORF starting with ATG of length 404 |
| | ID2747 | S | ORF starting with ATG of length 696 |
| | ID2748 | S | BH3142 PROTEIN. |
| 10 | ID2749 | S | ORF starting with ATG of length 316 |
| | ID2750 | S | BH2938 PROTEIN. |
| | ID2751 | S | TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF). |
| | ID2752 | S | BH0354 PROTEIN. |
| | ID2753 | S | BH3134 PROTEIN. |
| 15 | ID2754 | S | ORF starting with ATG of length 420 |
| | ID2755 | S | ORF starting with ATG of length 678 |
| | ID2756 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIC2 COMPONENT (EIIC2) |
| 20 | ID2757 | S | ORF starting with ATG of length 369 |
| | ID2758 | S | ORF starting with ATG of length 334 |
| | ID2759 | S | Staphylococcus aureus protein of unknown function. |
| | ID2760 | S | PROBABLE METHYLTRANSFERASE. |
| | ID2761 | S | ORF starting with ATG of length 1317 |
| | ID2762 | S | HYPOTHETICAL 15.9 KDA PROTEIN IN ILVD-THYB INTERGENIC |
| 25 | REGION | | |
| | ID2763 | S | THIOREDOXIN. |
| | ID2764 | S | OXIDOREDUCTASE (SHORT CHAIN DEHYDROGENASE/REDUCTASE FAMILY). |
| 30 | ID2765 | S | VIOMYCIN PHOSPHOTRANSFERASE (EC 2.7.1.103) (VIOMYCIN KINASE) |
| | ID2766 | S | ORF starting with ATG of length 534 |
| | ID2767 | S | BH3881 PROTEIN. |
| | ID2768 | S | RNA POLYMERASE ECF-TYPE SIGMA FACTOR. |
| | ID2769 | S | NA+/H ⁺ ANTIPORTER. |
| 35 | ID2770 | S | HYPOTHETICAL 51.3 KDA PROTEIN. |
| | ID2771 | S | BH2161 PROTEIN. |
| | ID2772 | S | ORF starting with ATG of length 240 |
| | ID2773 | S | HYPOTHETICAL 32.5 KDA PROTEIN IN CCCA-SODA INTERGENIC REGION |
| 40 | ID2774 | S | CHEMOTAXIS MOTA PROTEIN (MOTILITY PROTEIN A). |
| | ID2775 | S | UROPORPHYRINOGEN III SYNTHASE/METHYLTRANSFERASE (EC 4.2.1.75) |
| | ID2776 | S | BH3888 PROTEIN. |
| | ID2777 | S | ORF starting with ATG of length 483 |
| 45 | ID2778 | S | ORF starting with ATG of length 228 |
| | ID2779 | S | HYPOTHETICAL 43.6 KDA PROTEIN IN GBSA-TLPB INTERGENIC REGION |
| | ID2780 | S | YOKH PROTEIN. |
| | ID2781 | S | ORF starting with ATG of length 455 |
| 50 | ID2782 | S | Streptococcus pneumoniae encoded polypeptide. |
| | ID2783 | S | HYPOTHETICAL 14.9 KDA PROTEIN. |
| | ID2784 | S | Amino acid sequence of a Chlamydia pneumoniae protein. |
| | ID2785 | S | HYPOTHETICAL PROTEIN TC0114. |
| | ID2786 | S | C4-DICARBOXYLATE TRANSPORT SYSTEM (PERMEASE LARGE PROTEIN). |
| 55 | ID2787 | S | BH3131 PROTEIN. |
| | ID2788 | S | ORF starting with ATG of length 373 |
| | ID2789 | S | MULTIDRUG RESISTANCE PROTEIN. |
| | ID2790 | S | SIGMA-54-DEPENDENT TRANSCRIPTIONAL ACTIVATOR. |
| 60 | ID2791 | S | ORF starting with ATG of length 753 |
| | ID2792 | S | HYPOTHETICAL PROTEIN VC1334. |
| | ID2793 | S | CITS (TWO-COMPONENT SENSOR HISTIDINE KINASE). |
| | ID2794 | S | ASPARAGINE SYNTHETASE. |
| | ID2795 | S | YJDC PROTEIN. |
| 65 | ID2796 | S | HYPOTHETICAL 48.5 KDA PROTEIN. |
| | ID2797 | S | BH3666 PROTEIN. |

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| | ID2798 | S | ORF starting with ATG of length 684 |
| | ID2799 | S | BH1222 PROTEIN. |
| | ID2800 | S | PROBABLE POLY(A) POLYMERASE (EC 2.7.7.19) (PAP). |
| 5 | ID2801 | S | TRANSCRIPTIONAL REGULATOR (GNTR FAMILY). |
| | ID2802 | S | ORF starting with ATG of length 324 |
| | ID2803 | S | ORF starting with ATG of length 273 |
| | ID2804 | S | ORF starting with ATG of length 1043 |
| | ID2805 | S | BH0896 PROTEIN. |
| 10 | ID2806 | S | ALKALINE PHOSPHATASE LIKE PROTEIN. |
| | ID2807 | S | YFID (BH3304 PROTEIN). |
| | ID2808 | S | ORF starting with ATG of length 537 |
| | ID2809 | S | BH3040 PROTEIN. |
| | ID2810 | S | ORF starting with ATG of length 711 |
| | ID2811 | S | BH3040 PROTEIN. |
| 15 | ID2812 | S | HYPOTHETICAL 34.3 KDA PROTEIN. |
| | ID2813 | S | BH1235 PROTEIN. |
| | ID2814 | S | INVOLVED IN SPORE CORTEX SYNTHESIS. |
| | ID2815 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC ENZYME II, BC |
| | COMPONE | | |
| 20 | ID2816 | S | ORF starting with ATG of length 602 |
| | ID2817 | S | ORF starting with ATG of length 822 |
| | ID2818 | S | BH2596 PROTEIN. |
| | ID2819 | S | TRANSCRIPTIONAL REGULATOR (ICLR FAMILY). |
| | ID2820 | S | TRANSCRIPTIONAL ANTITERMINATOR. |
| 25 | ID2821 | S | BH2622 PROTEIN. |
| | ID2822 | S | ORF starting with ATG of length 465 |
| | ID2823 | S | ORF starting with ATG of length 390 |
| | ID2824 | S | ORF starting with ATG of length 226 |
| | ID2825 | S | ALPHA-MANNOSIDASE. |
| 30 | ID2826 | S | ORF starting with ATG of length 365 |
| | ID2827 | S | ORF starting with ATG of length 406 |
| | ID2828 | S | ORF starting with ATG of length 549 |
| | ID2829 | S | ORF starting with ATG of length 372 |
| | ID2830 | S | ORF starting with ATG of length 510 |
| 35 | ID2831 | S | ORF starting with ATG of length 1235 |
| | ID2832 | S | ORF starting with ATG of length 1418 |
| | ID2833 | S | ORF starting with ATG of length 825 |
| | ID2834 | S | PUTATIVE TRANSCRIPTION REGULATOR. |
| | ID2835 | S | ORF starting with ATG of length 593 |
| 40 | ID2836 | S | HYPOTHETICAL 16.3 KDA PROTEIN IN TGL-PGI INTERGENIC |
| | REGION. | | |
| | ID2837 | S | BH0852 PROTEIN. |
| | ID2838 | S | HYPOTHETICAL 15.0 KDA PROTEIN. |
| | ID2839 | S | TWO-COMPONENT RESPONSE REGULATOR. |
| 45 | ID2840 | S | YVRD PROTEIN. |
| | ID2841 | S | ORF starting with ATG of length 387 |
| | ID2842 | S | SERINE PROTEASE DO. |
| | ID2843 | S | BH4024 PROTEIN. |
| | ID2844 | S | STAGE V SPORULATION PROTEIN AD. |
| 50 | ID2845 | S | SIMILAR TO STAPHYLOCOCCUS AUREUS CAPA PROTEIN. |
| | ID2846 | S | YVBK PROTEIN. |
| | ID2847 | S | ORF starting with ATG of length 510 |
| | ID2848 | S | BH0988 PROTEIN. |
| | ID2849 | S | HYPOTHETICAL 9.7 KDA PROTEIN IN PURC-PURL INTERGENIC |
| 55 | REGION. | | |
| | ID2850 | S | ORF starting with ATG of length 890 |
| | ID2851 | S | ORF starting with ATG of length 381 |
| | ID2852 | S | HYPOTHETICAL OXIDOREDUCTASE IN GBSA-TLPB INTERGENIC |
| | REGION(E) | | |
| 60 | ID2853 | S | ORF starting with ATG of length 468 |
| | ID2854 | S | ORF starting with ATG of length 283 |
| | ID2855 | S | ORF starting with ATG of length 601 |
| | ID2856 | S | ORF starting with ATG of length 930 |
| | ID2857 | S | HYPOTHETICAL 25.4 KDA PROTEIN IN DPPE-HMP INTERGENIC |
| 65 | REGION. | | |
| | ID2858 | S | HYPOTHETICAL. |

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| | ID2859 | S | ORF starting with ATG of length 564 |
| | ID2860 | S | HOMOLOG OF PECTIN DEGRADING ENZYME 5-KETO 4- |
| | DEOXYURONATE ISO | | |
| 5 | ID2861 | S | ORF26. |
| | ID2862 | S | ORF starting with ATG of length 237 |
| | ID2863 | S | BH0236 PROTEIN. |
| | ID2864 | S | HYPOTHETICAL 33.9 KDA PROTEIN IN CRH-TRXB INTERGENIC |
| | REGION. | | |
| 10 | ID2865 | S | BH3568 PROTEIN. |
| | ID2866 | S | BH2633 PROTEIN. |
| | ID2867 | S | BH2637 PROTEIN. |
| | ID2868 | S | ORF starting with ATG of length 882 |
| | ID2869 | S | BH2252 PROTEIN. |
| 15 | ID2870 | S | HYPOTHETICAL 45.4 KDA PROTEIN IN THIAMINASE I |
| | 5'REGION. | | |
| | ID2871 | S | TRANSPOSAE (22). |
| | ID2872 | S | ABC TRANSPORTER (PERMEASE). |
| | ID2873 | S | PTS SYSTEM, FRUCTOSE-SPECIFIC IIABC COMPONENT. |
| 20 | ID2874 | S | PHOSPHOTRANSFERASE ENZYME II (EC 2.7.1.69) (PROTEIN- |
| | N(PI)-PHO | | |
| | ID2875 | S | BH3567 PROTEIN. |
| | ID2876 | S | ORF starting with ATG of length 306 |
| | ID2877 | S | BH2855 PROTEIN. |
| 25 | ID2878 | S | BH2638 PROTEIN. |
| | ID2879 | S | BH2637 PROTEIN. |
| | ID2880 | S | BH2284 PROTEIN. |
| | ID2881 | S | HYPOTHETICAL 100.1 KDA PROTEIN. |
| | ID2882 | S | BH2857 PROTEIN. |
| 30 | ID2883 | S | Endo-beta-N-acetylglucosaminidase A. |
| | ID2884 | S | BH0676 PROTEIN. |
| | ID2885 | S | BH1374 PROTEIN. |
| | ID2886 | S | C4-DICARBOXYLATE TRANSPORT SYSTEM (PERMEASE LARGE |
| | PROTEIN). | | |
| 35 | ID2887 | S | C4-DICARBOXYLATE TRANSPORT SYSTEM (PERMEASE LARGE |
| | PROTEIN). | | |
| | ID2888 | S | PUTATIVE METHYLTRANSFERASE. |
| | ID2889 | S | BH1465 PROTEIN. |
| | ID2890 | S | ORF starting with ATG of length 693 |
| | ID2891 | S | BH1921 PROTEIN. |
| 40 | ID2892 | S | E22 PROTEIN (GENE 43 PROTEIN). |
| | ID2893 | S | ORFZ (FRAGMENT). |
| | ID2894 | S | HYPOTHETICAL PROTEIN. |
| | ID2895 | S | ORF starting with ATG of length 791 |
| | ID2896 | S | BH0586 PROTEIN. |
| 45 | ID2897 | S | BH0587 PROTEIN. |
| | ID2898 | S | ORF starting with ATG of length 504 |
| | ID2899 | S | ORF starting with ATG of length 282 |
| | ID2900 | S | S. pneumoniae 30S ribosomal protein S2. |
| 50 | ID2901 | S | ORF starting with ATG of length 486 |
| | ID2902 | S | HYPOTHETICAL 39.5 KDA PROTEIN IN SIGZ-CSN INTERGENIC |
| | REGION. | | |
| | ID2903 | S | INDIRECT NEGATIVE REGULATOR OF SIGMA-B ACTIVITY |
| | (SERINE PHOS | | |
| 55 | ID2904 | S | DIHYDROLIPOAMIDE DEHYDROGENASE. |
| | ID2905 | S | ORF starting with ATG of length 399 |
| | ID2906 | S | MULTIDRUG RESISTANCE PROTEIN. |
| | ID2907 | S | BH2837 PROTEIN. |
| | ID2908 | S | ORF starting with ATG of length 387 |
| | ID2909 | S | ORF starting with ATG of length 362 |
| 60 | ID2910 | S | GERMINATION (CORTEX HYDROLYSIS) AND SPORULATION |
| | (STAGE II, M | | |
| | ID2911 | S | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN FEUA-SIGW |
| | INTERGEN | | |
| | ID2912 | S | YNGK PROTEIN. |
| 65 | ID2913 | S | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID2914 | S | BH1943 PROTEIN. |

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| | ID2915 | S | PENICILLIN-BINDING PROTEIN 1A (GERMINATION). |
| | ID2916 | S | BH2802 PROTEIN. |
| | ID2917 | S | BH1071 PROTEIN. |
| 5 | ID2918 | S | Corynebacterium glutamicum SMP protein sequence SEQ |
| | ID NO: 50 | | |
| | ID2919 | S | TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM). |
| | ID2920 | S | ORF starting with ATG of length 492 |
| | ID2921 | S | BH3562 PROTEIN. |
| | ID2922 | S | MODIFICATION METHYLASE CEQI (EC 2.1.1.72) (ADENINE- |
| 10 | SPECIFICM | | |
| | ID2923 | S | BH4007 PROTEIN. |
| | ID2924 | S | BH4008 PROTEIN. |
| | ID2925 | S | BH0058 PROTEIN. |
| | ID2926 | S | BH0589 PROTEIN. |
| 15 | ID2927 | S | ORF starting with ATG of length 297 |
| | ID2928 | S | BH3197 PROTEIN. |
| | ID2929 | S | PUTATIVE HOST CELL SURFACE-EXPOSED LIPOPROTEIN. |
| | ID2930 | S | BH0962 PROTEIN. |
| 20 | ID2931 | S | ORF starting with ATG of length 294 |
| | ID2932 | S | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID2933 | S | BH2007 PROTEIN. |
| | ID2934 | S | PENICILLIN TOLERANCE PROTEIN. |
| | ID2935 | S | BH3341 PROTEIN. |
| 25 | ID2936 | S | ORF starting with ATG of length 357 |
| | ID2937 | S | BH3829 PROTEIN. |
| | ID2938 | S | PUTATIVE SUGAR TRANSPORTER SUGAR BINDING PROTEIN. |
| | ID2939 | S | Nitrate reductase alpha chain protein. |
| | ID2940 | S | YETF PROTEIN. |
| 30 | ID2941 | S | SMALL, ACID-SOLUBLE SPORE PROTEIN D (SASP). |
| | ID2942 | S | BH4008 PROTEIN. |
| | ID2943 | S | YYDA PROTEIN. |
| | ID2944 | S | PUTATIVE REPLICATION FACTOR. |
| | ID2945 | S | ORF starting with ATG of length 570 |
| | ID2946 | S | ORF starting with ATG of length 389 |
| 35 | ID2947 | S | SPORULATION INITIATION PHOSPHOPROTEIN. |
| | ID2948 | S | ORF starting with ATG of length 388 |
| | ID2949 | S | XYLOSIDASE/ARABINOSIDASE. |
| | ID2950 | S | HYPOTHETICAL 56.0 KDA PROTEIN IN GLGB-GBSB INTERGENIC |
| | REGION | | |
| 40 | ID2951 | S | ALKALINE PHOSPHATASE. |
| | ID2952 | S | ORF starting with ATG of length 231 |
| | ID2953 | S | BH3404 PROTEIN. |
| | ID2954 | S | BH3402 PROTEIN. |
| | ID2955 | S | ORF starting with ATG of length 420 |
| 45 | ID2956 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC ENZYME II, C2 |
| | COMPONE | | |
| | ID2957 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC ENZYME II, BC |
| | COMPONE | | |
| | ID2958 | S | ORF starting with ATG of length 469 |
| 50 | ID2959 | S | ORF, HYPOTHETICAL PROTEIN. |
| | ID2960 | S | YFHO PROTEIN. |
| | ID2961 | S | HYPOTHETICAL 13.1 KDA PROTEIN C29B12.12 IN CHROMOSOME |
| | I. | | |
| | ID2962 | S | BH1053 PROTEIN. |
| 55 | ID2963 | S | ENOYL- [ACYL-CARRIER PROTEIN] REDUCTASE. |
| | ID2964 | S | BH2840 PROTEIN. |
| | ID2965 | S | X-LINKED RETINOPATHY PROTEIN (FRAGMENT). |
| | ID2966 | S | TRANSPORTER. |
| | ID2967 | S | Staphylococcus aureus protein of unknown function. |
| 60 | ID2968 | S | CYTIDINE DEAMINASE (EC 3.5.4.5). |
| | ID2969 | S | BH0315 PROTEIN. |
| | ID2970 | S | SMALL CORE PROTEIN (J PROTEIN). |
| | ID2971 | S | SCAFFOLDING PROTEIN D (GPD). |
| | ID2972 | S | CAPSID PROTEIN (F PROTEIN) (GPF). |
| 65 | ID2973 | S | BH1682 PROTEIN. |
| | ID2974 | S | 50S RIBOSOMAL PROTEIN L30. |

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| | ID2975 | S | ORF starting with ATG of length 519 |
| | ID2976 | S | BH2274 PROTEIN. |
| | ID2977 | S | ORF starting with ATG of length 336 |
| | ID2978 | S | ORF starting with ATG of length 588 |
| 5 | ID2979 | S | BH2981 PROTEIN. |
| | ID2980 | S | BH1804 PROTEIN. |
| | ID2981 | S | HYPOTHETICAL PROTEIN VC1332. |
| | ID2982 | S | ORF starting with ATG of length 333 |
| | ID2983 | S | BH3423 PROTEIN. |
| 10 | ID2984 | S | BH3430 PROTEIN. |
| | ID2985 | S | ORF starting with ATG of length 600 |
| | ID2986 | S | BH1089 PROTEIN. |
| | ID2987 | S | BH1707 PROTEIN. |
| | ID2988 | S | ORF starting with ATG of length 360 |
| 15 | ID2989 | S | YUBB PROTEIN. |
| | ID2990 | S | YNGK PROTEIN. |
| | ID2991 | S | YTER. |
| | ID2992 | S | TRANSCRIPTION ANTITERMINATOR. |
| | ID2993 | S | BH1883 PROTEIN. |
| 20 | ID2994 | S | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTE |
| | ID2995 | S | ORF starting with ATG of length 389 |
| | ID2996 | S | BH1336 PROTEIN. |
| | ID2997 | S | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| 25 | ID2998 | S | ORF starting with ATG of length 498 |
| | ID2999 | S | THYMIDINE KINASE (EC 2.7.1.21). |
| | ID3000 | S | YVRI PROTEIN. |
| | ID3001 | S | ORF starting with ATG of length 270 |
| | ID3002 | S | ORF starting with ATG of length 486 |
| 30 | ID3003 | S | HYPOTHETICAL 11.0 KDA PROTEIN IN HSP18 3'REGION (ORFA1). |
| | ID3004 | S | BH0973 PROTEIN. |
| | ID3005 | S | BH0974 PROTEIN. |
| | ID3006 | S | Cyclohexanone monooxygenase sequence. |
| 35 | ID3007 | S | HYPOTHETICAL 76.9 KDA PROTEIN. |
| | ID3008 | S | MN CATALASE. |
| | ID3009 | S | SA0330 PROTEIN. |
| | ID3010 | S | ORNITHINE CARBAMOYLTRANSFERASE. |
| | ID3011 | S | ACETOIN DEHYDROGENASE. |
| 40 | ID3012 | S | ORF starting with ATG of length 258 |
| | ID3013 | S | HYPOTHETICAL 6.4 KDA PROTEIN. |
| | ID3014 | S | HYPOTHETICAL 48.6 KDA PROTEIN IN SERS-DNAZ INTERGENIC REGION |
| | ID3015 | S | MINOR TEICHOIC ACIDS BIOSYNTHESIS PROTEIN GGAA. |
| 45 | ID3016 | S | HYPOTHETICAL PROTEIN XF1280. |
| | ID3017 | S | ORF starting with ATG of length 472 |
| | ID3018 | S | BH3318 PROTEIN. |
| | ID3019 | S | ORF starting with ATG of length 618 |
| | ID3020 | S | Bacillus clausii NN049095 BXN20 beta-1,4-mannanase precursor |
| 50 | ID3021 | S | ORF starting with ATG of length 474 |
| | ID3022 | S | HYPOTHETICAL 4.8 KDA PROTEIN. |
| | ID3023 | S | HYPOTHETICAL 8.0 KDA PROTEIN. |
| | ID3024 | S | SPORE COAT PROTEIN X (INSOLUBLE FRACTION). |
| 55 | ID3025 | S | TRANSCRIPTIONAL REGULATOR. |
| | ID3026 | S | ORF starting with ATG of length 771 |
| | ID3027 | S | DAUNORUBICIN RESISTANCE PROTEIN. |
| | ID3028 | S | MLL2253 PROTEIN. |
| | ID3029 | S | ORF starting with ATG of length 495 |
| 60 | ID3030 | S | ORF starting with ATG of length 402 |
| | ID3031 | S | SPAG. |
| | ID3032 | S | YOLA. |
| | ID3033 | S | S. pneumoniae diacylglycerol kinase. |
| | ID3034 | S | CHORISMATE MUTASE. |
| 65 | ID3035 | S | TRANSCRIPTIONAL ANTITERMINATOR. |
| | ID3036 | S | TRANSCRIPTIONAL REGULATOR (LYSR FAMILY). |

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| | ID3037 | S | HYPOTHETICAL 37.5 KDA PROTEIN (FRAGMENT). |
| | ID3038 | S | BH0105 PROTEIN. |
| | ID3039 | S | GLYCEROL-3-PHOSPHATE CYTIDYLTRANSFERASE. |
| | ID3040 | S | BH1230 PROTEIN. |
| 5 | ID3041 | S | ORF starting with ATG of length 456 |
| | ID3042 | S | Streptococcus pneumoniae encoded polypeptide. |
| | ID3043 | S | HYPOTHETICAL 14.9 KDA PROTEIN. |
| | ID3044 | S | Amino acid sequence of a Chlamydia pneumoniae protein. |
| | ID3045 | S | HYPOTHETICAL PROTEIN TC0114. |
| 10 | ID3046 | S | CATION TRANSPORT ATPASE, E1-E2 FAMILY. |
| | ID3047 | S | MLL1121 PROTEIN. |
| | ID3048 | S | BH1620 PROTEIN. |
| | ID3049 | S | ORF starting with ATG of length 386 |
| | ID3050 | S | BH2390 PROTEIN. |
| 15 | ID3051 | S | ORF starting with ATG of length 294 |
| | ID3052 | S | ID867. |
| | ID3053 | S | VALYL-TRNA SYNTHETASE (EC 6.1.1.9). |
| | ID3054 | S | BH0488 PROTEIN. |
| | ID3055 | S | ORF starting with ATG of length 844 |
| 20 | ID3056 | S | BH1492 PROTEIN. |
| | ID3057 | S | ORF starting with ATG of length 366 |
| | ID3058 | S | BH2821 PROTEIN. |
| | ID3059 | S | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID3060 | S | BH1550 PROTEIN. |
| 25 | ID3061 | S | BH2938 PROTEIN. |
| | ID3062 | S | PXO1-37. |
| | ID3063 | S | BH3176 PROTEIN. |
| | ID3064 | S | HYPOTHETICAL 50.9 KDA PROTEIN IN KATA 3'REGION (ORF A). |
| 30 | ID3065 | S | ORF starting with ATG of length 534 |
| | ID3066 | S | BH3627 PROTEIN. |
| | ID3067 | S | ORF starting with ATG of length 558 |
| | ID3068 | S | ORF starting with ATG of length 632 |
| | ID3069 | S | ORF starting with ATG of length 650 |
| 35 | ID3070 | S | L-RHAMNOSE ISOMERASE. |
| | ID3071 | S | BH2412 PROTEIN. |
| | ID3072 | S | DNA TRANSPORT MACHINERY. |
| | ID3073 | S | BH0051 PROTEIN. |
| | ID3074 | S | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| 40 | ID3075 | S | PXO1-37. |
| | ID3076 | S | ORF starting with ATG of length 588 |
| | ID3077 | S | IMMUNOGENIC PROTEIN. |
| | ID3078 | S | ORF starting with ATG of length 518 |
| | ID3079 | S | BH1232 PROTEIN. |
| 45 | ID3080 | S | SENSOR HISTIDINE KINASE CHEA. |
| | ID3081 | S | REPRESSOR. |
| | ID3082 | S | BH2052 PROTEIN. |
| | ID3083 | S | SSPF PROTEIN. |
| | ID3084 | S | ORF starting with ATG of length 279 |
| 50 | ID3085 | S | ORF starting with ATG of length 569 |
| | ID3086 | S | ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27). |
| | ID3087 | S | SPORE GERMINATION PROTEIN A1. |
| | ID3088 | S | MUTANTS BLOCK SPORULATION AFTER ENGULFMENT. |
| | ID3089 | S | MUTANTS BLOCK SPORULATION AFTER ENGULFMENT. |
| 55 | ID3090 | S | ORF starting with ATG of length 272 |
| | ID3091 | S | SPORE GERMINATION PROTEIN KC. |
| | ID3092 | S | YBFO PROTEIN. |
| | ID3093 | S | PEPTIDASE. |
| | ID3094 | S | ORF starting with TTG or GTG of length 573 |
| 60 | ID3095 | S | SODIUM-DEPENDENT PHOSPHATE TRANSPORTER. |
| | ID3096 | S | HYPOTHETICAL 41.4 KDA PROTEIN IN IADA-MCRD INTERGENIC REGION |
| | ID3097 | S | STAGE III SPORULATION PROTEIN AE. |
| | ID3098 | S | STAGE III SPORULATION PROTEIN AF. |
| 65 | ID3099 | S | BH0266 PROTEIN. |
| | ID3100 | S | BH2381 PROTEIN. |

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| | ID3101 | S | ORF starting with ATG of length 312 |
| | ID3102 | S | BH0315 PROTEIN. |
| | ID3103 | S | PUTATIVE RNA POLYMERASE SIGMA FACTOR. |
| | ID3104 | S | BH3310 PROTEIN. |
| 5 | ID3105 | S | HYPOTHETICAL 18.1 KDA PROTEIN. |
| | ID3106 | S | HYPOTHETICAL 44.9 KDA PROTEIN. |
| | ID3107 | S | GLYCEROL UPTAKE OPERON ANTITERMINATOR REGULATORY |
| | PROTEIN. | | |
| 10 | ID3108 | S | CDNA FLJ20489 FIS, CLONE KAT08285. |
| | ID3109 | S | CREATINE KINASE. |
| | ID3110 | S | YVRH PROTEIN (RECEIVER MODULE OF PUTATIVE RESPONSE |
| | REGULATOR | | |
| | ID3111 | S | YFIT PROTEIN. |
| 15 | ID3112 | S | BH3588 PROTEIN. |
| | ID3113 | S | YFIT PROTEIN. |
| | ID3114 | S | YRVE PROTEIN. |
| | ID3115 | S | BH1239 PROTEIN. |
| | ID3116 | S | ORF starting with ATG of length 379 |
| | ID3117 | S | BH2912 PROTEIN. |
| 20 | ID3118 | S | BH0043 PROTEIN. |
| | ID3119 | S | BH3320 PROTEIN. |
| | ID3120 | S | BH3319 PROTEIN. |
| | ID3121 | S | BH1498 PROTEIN. |
| | ID3122 | S | DNA POLYMERASE III DELTA' SUBUNIT (EC 2.7.7.7). |
| 25 | ID3123 | S | SIGNAL PEPTIDASE-LIKE PROTEIN. |
| | ID3124 | S | ORF starting with ATG of length 435 |
| | ID3125 | S | Human secreted protein sequence encoded by gene 45 |
| | SEQ ID NO | | |
| 30 | ID3126 | S | Human secreted protein, SEQ ID NO: 7174. |
| | ID3127 | S | ORFII. |
| | ID3128 | S | BH1265 PROTEIN. |
| | ID3129 | S | BH1264 PROTEIN. |
| | ID3130 | S | FLAGELLAR BIOSYNTHETIC PROTEIN FLIZ PRECURSOR. |
| | ID3131 | S | ORF starting with ATG of length 498 |
| 35 | ID3132 | S | MOLYBDOPTERIN CONVERTING FACTOR (SUBUNIT 1). |
| | ID3133 | S | BH4017 PROTEIN. |
| | ID3134 | S | PUTATIVE HSDS. |
| | ID3135 | S | ORF starting with TTG or GTG of length 534 |
| | ID3136 | S | D-FRUCTOSE-1,6-BIPHOSPHATE ALDOLASE (FRAGMENT). |
| 40 | ID3137 | S | BH1341 PROTEIN. |
| | ID3138 | S | STAGE II SPORULATION PROTEIN P. |
| | ID3139 | S | BH1765 PROTEIN. |
| | ID3140 | S | BH3095 PROTEIN. |
| | ID3141 | S | YFNK. |
| 45 | ID3142 | S | SPORE GERMINATION PROTEIN. |
| | ID3143 | S | ORF starting with ATG of length 336 |
| | ID3144 | S | NA+/H+ ANTIPORTER. |
| | ID3145 | S | ORF starting with ATG of length 645 |
| | ID3146 | S | PUTATIVE RESPONSE REGULATOR. |
| 50 | ID3147 | S | ORF starting with ATG of length 558 |
| | ID3148 | S | 2-KETO-3-DEOXYGLUCONATE PERMEASE (KDG PERMEASE). |
| | ID3149 | S | BH0802 PROTEIN. |
| | ID3150 | S | BH0285 PROTEIN. |
| | ID3151 | S | ORF starting with ATG of length 287 |
| 55 | ID3152 | S | HYPOTHETICAL 30.6 KDA PROTEIN (ORF266). |
| | ID3153 | S | STAGE II SPORULATION PROTEIN M. |
| | ID3154 | S | YFNK. |
| | ID3155 | S | TRANSCRIPTION ANTITERMINATOR. |
| | ID3156 | S | Human secreted protein, SEQ ID NO: 7519. |
| 60 | ID3157 | S | 5-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24). |
| | ID3158 | S | GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) |
| | (GLUCOSAMINE | | |
| | ID3159 | S | PUTATIVE TETR-FAMILY TRANSCRIPTIONAL REGULATOR. |
| | ID3160 | S | ABC TRANSPORTER (ATP-BINDING PROTEIN). |
| 65 | ID3161 | S | YLBM PROTEIN. |
| | ID3162 | S | GLYCINE BETAINE TRANSPORTER. |

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| | ID3163 | S | INTEGRASE HOMOLOG. |
| | ID3164 | S | ORF starting with ATG of length 300 |
| | ID3165 | S | ORF starting with ATG of length 259 |
| 5 | ID3166 | S | PUTATIVE XYLOSE OPERON REGULATORY PROTEIN. |
| | ID3167 | S | ORF starting with ATG of length 256 |
| | ID3168 | S | CELL WALL LYtic ACTIVITY. |
| | ID3169 | S | BH3591 PROTEIN. |
| | ID3170 | S | YTOQ. |
| 10 | ID3171 | S | SPORE GERMINATION PROTEIN. |
| | ID3172 | S | ORF starting with ATG of length 692 |
| | ID3173 | S | ORF starting with ATG of length 459 |
| | ID3174 | S | ALKYL HYDROPEROXIDE REDUCTASE LARGE SUBUNIT (EC 1.6.99.3) (P) |
| 15 | ID3175 | S | MOLYBDOPTERIN BIOSYNTHESIS. |
| | ID3176 | S | NA(+) / H(+) ANTIPORTER (SODIUM/PROTON ANTIPORTER). |
| | ID3177 | S | ORF starting with ATG of length 480 |
| | ID3178 | S | OLIGOPEPTIDE ABC TRANSPORTER (PERMEASE). |
| | ID3179 | S | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| 20 | ID3180 | S | ORF starting with TTG or GTG of length 1386 |
| | ID3181 | S | HYPOTHETICAL 29.1 KDA PROTEIN. |
| | ID3182 | S | Streptococcus pneumoniae type 4 protein sequence #75. |
| | ID3183 | S | SPORE GERMINATION PROTEIN. |
| | ID3184 | S | ORF starting with ATG of length 351 |
| 25 | ID3185 | S | SPORE GERMINATION PROTEIN KA. |
| | ID3186 | S | ORF starting with ATG of length 274 |
| | ID3187 | S | SPORE GERMINATION PROTEIN. |
| | ID3188 | S | ORF starting with ATG of length 266 |
| | ID3189 | S | ORF13. |
| 30 | ID3190 | S | KYNURENINASE (EC 3.7.1.3) (L-KYNURENINE HYDROLASE). |
| | ID3191 | S | BH0970 PROTEIN. |
| | ID3192 | S | ORF starting with ATG of length 434 |
| | ID3193 | S | ORF starting with ATG of length 735 |
| | ID3194 | S | MLL3044 PROTEIN. |
| 35 | ID3195 | S | HYPOTHETICAL OXIDOREDUCTASE IN RTP-PELB INTERGENIC REGION (E) |
| | ID3196 | S | HYPOTHETICAL 47.4 KDA PROTEIN. |
| | ID3197 | S | ORF starting with ATG of length 554 |
| | ID3198 | S | ORF starting with ATG of length 372 |
| | ID3199 | S | ORF starting with ATG of length 300 |
| 40 | ID3200 | S | BH2631 PROTEIN. |
| | ID3201 | S | HYPOTHETICAL 8.2 KDA PROTEIN IN NPRE-PYCA INTERGENIC REGION. |
| | ID3202 | S | ORF starting with ATG of length 279 |
| | ID3203 | S | BH0602 PROTEIN. |
| 45 | ID3204 | S | YFKK PROTEIN. |
| | ID3205 | S | HYPOTHETICAL 35.5 KDA PROTEIN. |
| | ID3206 | S | ORF starting with ATG of length 696 |
| | ID3207 | S | BH0717 PROTEIN. |
| | ID3208 | S | BH3320 PROTEIN. |
| 50 | ID3209 | S | ORF11. |
| | ID3210 | S | TRANSCRIPTIONAL ACTIVATOR OF THE GLUTAMATE SYNTHASE OPERON (|
| | ID3211 | S | ORF starting with ATG of length 347 |
| | ID3212 | S | FERRICHROME TRANSPORT PERMEASE. |
| 55 | ID3213 | S | TRANSCRIPTIONAL REGULATOR. |
| | ID3214 | S | CELL DIVISION CYCLE CDC48 HOMOLOG (YJOB PROTEIN). |
| | ID3215 | S | PUTATIVE SECRETED PROTEIN. |
| | ID3216 | S | TYPE I RESTRICTION ENZYME ECOKI M PROTEIN (EC 2.1.1.72) (M.E) |
| 60 | ID3217 | S | A2-5A ORF1 (FRAGMENT). |
| | ID3218 | S | PHI PVL ORF 63 HOMOLOGUE. |
| | ID3219 | S | ORF starting with ATG of length 477 |
| | ID3220 | S | ORF22. |
| | ID3221 | S | URIDYL KINASE (EC 2.7.1.48) (URIDYL |
| 65 | MONOPHOSPHOKINASE). | | |
| | ID3222 | S | HYPOTHETICAL 30.7 KDA PROTEIN. |

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| | ID3223 | S | BH3410 PROTEIN. |
| | ID3224 | S | PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN |
| | YCKA. | | |
| | ID3225 | S | HYPOTHETICAL PROTEIN. |
| 5 | ID3226 | S | TRANSCRIPTION REGULATOR. |
| | ID3227 | S | SERINE/THREONINE PROTEIN KINASE. |
| | ID3228 | S | ORF starting with ATG of length 960 |
| | ID3229 | S | ORF starting with TTG or GTG of length 561 |
| | ID3230 | S | ORF11. |
| 10 | ID3231 | S | PTS SYSTEM, SUCROSE PHOSPHOTRANSFERASE ENZYME II, BC |
| | COMPONE | | |
| | ID3232 | S | HYPOTHETICAL PROTEIN. |
| | ID3233 | S | GERMINATION PROTEIN. |
| | ID3234 | S | DIAMINOBUTYRIC ACID ACETYLTRANSFERASE. |
| 15 | ID3235 | S | Staphylococcus aureus protein of unknown function. |
| | ID3236 | S | HYPOTHETICAL 38.4 KDA PROTEIN. |
| | ID3237 | S | RELATED TO A-AGGLUTININ CORE PROTEIN AGA1. |
| | ID3238 | S | DEACETYLASE, PUTATIVE. |
| 20 | ID3239 | S | E. coli aspartokinase III variant No.169 (T352I, S369F). |
| | ID3240 | S | BH1501 PROTEIN. |
| | ID3241 | S | BH2389 PROTEIN. |
| | ID3242 | S | ORF starting with ATG of length 278 |
| | ID3243 | S | PROBABLE TWO-COMPONENT SENSOR. |
| 25 | ID3244 | S | BH0892 PROTEIN. |
| | ID3245 | S | BH1268 PROTEIN. |
| | ID3246 | S | BH1270 PROTEIN. |
| | ID3247 | S | ORF starting with ATG of length 969 |
| | ID3248 | S | ORF starting with ATG of length 312 |
| 30 | ID3249 | S | ABC TRANSPORTER (ATP-BINDING PROTEIN) (DAUNORUBICIN |
| | RESISTAN | | |
| | ID3250 | S | Streptococcus pneumoniae SP0014 protein. |
| | ID3251 | S | L-ASPARTATE OXIDASE (EC 1.4.3.16) (QUINOLINATE |
| | SYNTHETASE B) | | |
| 35 | ID3252 | S | BH2905 PROTEIN. |
| | ID3253 | S | INNER SPORE COAT PROTEIN D. |
| | ID3254 | S | ORF starting with ATG of length 237 |
| | ID3255 | S | ORF starting with ATG of length 452 |
| | ID3256 | S | REGULATORY PROTEIN BLARI. |
| 40 | ID3257 | S | ORF starting with ATG of length 1200 |
| | ID3258 | S | ORF starting with ATG of length 219 |
| | ID3259 | S | BH1892 PROTEIN. |
| | ID3260 | S | ORF starting with ATG of length 624 |
| | ID3261 | S | INTEGRASE HOMOLOG. |
| 45 | ID3262 | S | HYPOTHETICAL 7.6 KDA PROTEIN. |
| | ID3263 | S | HYPOTHETICAL 40.9 KDA PROTEIN IN CCCA-SODA INTERGENIC |
| | REGION | | |
| | ID3264 | S | BH1955 PROTEIN. |
| | ID3265 | S | TRANSCRIPTIONAL REGULATOR OF SPORE COAT PROTEIN |
| 50 | (SPORE GERM | | |
| | ID3266 | S | BH3205 PROTEIN. |
| | ID3267 | S | BH1176 PROTEIN. |
| | ID3268 | S | BH1402 PROTEIN. |
| | ID3269 | S | LACZ ALPHA PEPTIDE. |
| 55 | ID3270 | S | TRANSCRIPTIONAL REGULATOR OF SPORE COAT PROTEIN |
| | (SPORE GERM | | |
| | ID3271 | S | BH2907 PROTEIN. |
| | ID3272 | S | BH2908 PROTEIN. |
| | ID3273 | S | STAGE II SPORULATION PROTEIN R. |
| 60 | ID3274 | S | BH1678 PROTEIN. |
| | ID3275 | S | BICYCLOMYCIN RESISTANCE PROTEIN. |
| | ID3276 | S | Synechocystis sp phytochrome-related gene Cph1. |
| | ID3277 | S | ORF starting with ATG of length 222 |
| | ID3278 | S | BH3205 PROTEIN. |
| 65 | ID3279 | S | BH0535 PROTEIN. |
| | ID3280 | S | HYPOTHETICAL PROTEIN TC0114. |

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| | ID3281 | S | Amino acid sequence of a Chlamydia pneumoniae protein. |
| | ID3282 | S | HYPOTHETICAL 14.9 KDA PROTEIN. |
| | ID3283 | S | Streptococcus pneumoniae encoded polypeptide. |
| 5 | ID3284 | S | ORF starting with ATG of length 456 |
| | ID3285 | S | HYPOTHETICAL 6.9 KDA PROTEIN APES063. |
| | ID3286 | S | Chlamydia pneumoniae lipoprotein sequence. |
| | ID3287 | S | ORF starting with ATG of length 411 |
| | ID3288 | S | BH0407 PROTEIN. |
| | ID3289 | S | BH3604 PROTEIN. |
| 10 | ID3290 | S | CAPSULAR POLYSACCHARIDE BIOSYNTHESIS. |
| | ID3291 | S | BH3874 PROTEIN. |
| | ID3292 | S | ORF starting with ATG of length 501 |
| | ID3293 | S | BETA-N-ACETYLGLUCOSAMINIDASE PRECURSOR (EC 3.2.1.-). |
| 15 | ID3294 | S | Chlamydia pneumoniae lipoprotein sequence. |
| | ID3295 | S | HYPOTHETICAL 6.9 KDA PROTEIN APES063. |
| | ID3296 | S | ORF starting with ATG of length 456 |
| | ID3297 | S | Streptococcus pneumoniae encoded polypeptide. |
| | ID3298 | S | HYPOTHETICAL 14.9 KDA PROTEIN. |
| 20 | ID3299 | S | Amino acid sequence of a Chlamydia pneumoniae protein. |
| | ID3300 | S | HYPOTHETICAL PROTEIN TC0114. |
| | ID3301 | S | Chlamydia pneumoniae lipoprotein sequence. |
| | ID3302 | S | YHCG (ABC TRANSPORTER) (ATP-BINDING PROTEIN). |
| | ID3303 | S | SPOIISA PROTEIN. |
| 25 | ID3304 | S | BH1232 PROTEIN. |
| | ID3305 | S | TRANSPOSSASE (11). |
| | ID3306 | S | ORF starting with ATG of length 462 |
| | ID3307 | S | ORF starting with ATG of length 672 |
| | ID3308 | S | RESPONSE REGULATOR ASPARTATE PHOSPHATASE. |
| 30 | ID3309 | S | HYPOTHETICAL 56.9 KDA PROTEIN PH1047. |
| | ID3310 | S | BH0590 PROTEIN. |
| | ID3311 | S | RYBOFLAVIN BIOSYNTHESIS PROTEIN RIBA [INCLUDES: GTP CYCLOHYD |
| | ID3312 | S | HYPOTHETICAL 21.0 KDA PROTEIN IN CTAF 3' REGION (ORF1). |
| 35 | ID3313 | S | HYPOTHETICAL 17.8 KDA PROTEIN IN CTAF 3' REGION (ORF3). |
| | ID3314 | S | BH1678 PROTEIN. |
| | ID3315 | S | ORF starting with ATG of length 384 |
| | ID3316 | S | BH2622 PROTEIN. |
| 40 | ID3317 | S | STAGE IV SPORULATION PROTEIN A (SPORE CORTEX FORMATION AND C |
| | ID3318 | S | ORF, HYPOTHETICAL PROTEIN. |
| | ID3319 | S | INTRACELLULAR PROTEINASE (EC 3.2.). |
| 45 | ID3320 | S | RETINITIS PIGMENTOSA GTPASE REGULATOR-LIKE PROTEIN (FRAGMENT |
| | ID3321 | S | ORF22. |
| | ID3322 | S | BH1644 PROTEIN. |
| | ID3323 | S | BH0861 PROTEIN. |
| | ID3324 | S | MEMBRANE-TYPE MOSAIC SERINE PROTEASE. |
| 50 | ID3325 | S | ORF starting with ATG of length 488 |
| | ID3326 | S | BH1720 PROTEIN. |
| | ID3327 | S | HYPOTHETICAL 20.5 KDA PROTEIN. |
| | ID3328 | S | YFIL. |
| | ID3329 | S | BH3604 PROTEIN. |
| 55 | ID3330 | S | SPORE GERMINATION PROTEIN. |
| | ID3331 | S | ORF starting with ATG of length 1109 |
| | ID3332 | S | BH0842 PROTEIN. |
| | ID3333 | S | AMINO ACID ABC TRANSPORTER PROTEIN, SOLUTE-BINDING COMPONENT |
| 60 | ID3334 | S | BH0589 PROTEIN. |
| | ID3335 | S | YFKB PROTEIN. |
| | ID3336 | S | BH0883 PROTEIN. |
| | ID3337 | S | BH3772 PROTEIN. |
| | ID3338 | S | STAGE II SPORULATION PROTEIN R. |
| 65 | ID3339 | S | ORF starting with ATG of length 255 |
| | ID3340 | S | ORF26. |

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| | ID3341 | S | ORF25. |
| | ID3342 | S | ORF16. |
| | ID3343 | S | ORF starting with ATG of length 1107 |
| | ID3344 | S | BH1721 PROTEIN. |
| 5 | ID3345 | S | YJBK PROTEIN. |
| | ID3346 | S | BH2850 PROTEIN. |
| | ID3347 | S | GTP PYROPHOSPHOKINASE. |
| | ID3348 | S | NAD KINASE. |
| | ID3349 | S | BH2209 PROTEIN. |
| 10 | ID3350 | S | BH2208 PROTEIN. |
| | ID3351 | S | YVMA. |
| | ID3352 | S | BH1114 PROTEIN. |
| | ID3353 | S | TRANSCRIPTION REGULATOR. |
| 15 | ID3354 | S | FRUCTOSE 1-PHOSPHATE KINASE. |
| | ID3355 | S | ORF starting with ATG of length 782 |
| | ID3356 | S | ORF starting with ATG of length 466 |
| | ID3357 | S | HYPOTHETICAL 22.4 KDA PROTEIN IN RPMF-FTSL INTERGENIC REGION |
| | ID3358 | S | BH2580 PROTEIN. |
| 20 | ID3359 | S | ORF starting with ATG of length 324 |
| | ID3360 | S | HYPOTHETICAL 48.9 KDA PROTEIN PH0207. |
| | ID3361 | S | SPORE CORTEX-LYTIC ENZYME. |
| | ID3362 | S | HYPOTHETICAL 62.6 KDA PROTEIN IN RPMF-FTSL INTERGENIC REGION |
| 25 | ID3363 | S | ORF starting with ATG of length 393 |
| | ID3364 | S | ORF starting with ATG of length 405 |
| | ID3365 | S | ORF starting with ATG of length 294 |
| | ID3366 | S | BH4024 PROTEIN. |
| | ID3367 | S | RESOLVASE. |
| 30 | ID3368 | S | BLMT. |
| | ID3369 | S | ORF starting with ATG of length 285 |
| | ID3370 | S | BH0236 PROTEIN. |
| | ID3371 | S | BH0942 PROTEIN. |
| | ID3372 | S | ORF starting with ATG of length 339 |
| 35 | ID3373 | S | ORF starting with ATG of length 424 |
| | ID3374 | S | PHAGE-RELATED PROTEIN. |
| | ID3375 | S | BH1913 PROTEIN. |
| | ID3376 | S | HYPOTHETICAL 19.4 KDA PROTEIN IN SPOIIR-GLYC INTERGENIC REGI |
| 40 | ID3377 | S | BH1404 PROTEIN. |
| | ID3378 | S | OUTER SPORE COAT PROTEIN. |
| | ID3379 | S | HYPOTHETICAL 28.2 KDA PROTEIN IN BIOI 3'REGION (ORF2). |
| | ID3380 | S | ORF starting with ATG of length 537 |
| 45 | ID3381 | S | MLR2098 PROTEIN. |
| | ID3382 | S | RELATED TO DIMERIC DIHYDRODIOL DEHYDROGENASE. |
| | ID3383 | S | PUTATIVE FRUCTOSE-SPECIFIC PERMEASE. |
| | ID3384 | S | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3385 | S | SIGMA 54 ACTIVATOR. |
| 50 | ID3386 | S | ORF starting with ATG of length 331 |
| | ID3387 | S | BH0913 PROTEIN. |
| | ID3388 | S | BH2208 PROTEIN. |
| | ID3389 | S | ORF starting with ATG of length 414 |
| | ID3390 | S | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627. |
| 55 | ID3391 | S | BH1722 PROTEIN. |
| | ID3392 | S | HYPOTHETICAL 39.0 KDA PROTEIN. |
| | ID3393 | S | ORF starting with ATG of length 315 |
| | ID3394 | S | BH3770 PROTEIN. |
| | ID3395 | S | BH1676 PROTEIN. |
| 60 | ID3396 | S | ORF45. |
| | ID3397 | S | ORF starting with ATG of length 436 |
| | ID3398 | S | PUTATIVE INTEGRAL MEMBRANE TRANSPORTER. |
| | ID3399 | S | BH1148 PROTEIN. |
| | ID3400 | S | BH1812 PROTEIN. |
| 65 | ID3401 | S | TYROSYL-TRNA SYNTHETASE 2 (EC 6.1.1.1) (TYROSINE-- TRNA LIGAS |

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| | ID3402 | S | BH0365 PROTEIN. |
| | ID3403 | S | BH2667 PROTEIN. |
| | ID3404 | S | PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC COMPONENT (EIIDC) |
| 5 | ID3405 | S | ORF starting with ATG of length 702 |
| | ID3406 | S | BH4015 PROTEIN. |
| | ID3407 | S | BH0346 PROTEIN. |
| | ID3408 | S | ORF starting with ATG of length 335 |
| | ID3409 | S | ORF starting with ATG of length 350 |
| 10 | ID3410 | S | ORF starting with ATG of length 506 |
| | ID3411 | S | ORF starting with ATG of length 621 |
| | ID3412 | S | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN OPUE-RAPH INTERGEN |
| | ID3413 | S | BH1410 PROTEIN. |
| 15 | ID3414 | S | ORF starting with ATG of length 346 |
| | ID3415 | S | ORF starting with ATG of length 542 |
| | ID3416 | S | DAUNORUBICIN RESISTANCE PROTEIN. |
| | ID3417 | S | BH2291 PROTEIN. |
| 20 | ID3418 | S | ORF starting with ATG of length 645 |
| | ID3419 | S | BH3410 PROTEIN. |
| | ID3420 | S | PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN YCKA. |
| | ID3421 | S | ORF starting with ATG of length 696 |
| | ID3422 | S | NITRIC OXIDE SYNTHASE. |
| 25 | ID3423 | S | BH3568 PROTEIN. |
| | ID3424 | S | BH3567 PROTEIN. |
| | ID3425 | S | MLR2098 PROTEIN. |
| | ID3426 | S | ORF starting with ATG of length 396 |
| | ID3427 | S | ORF starting with ATG of length 945 |
| 30 | ID3428 | S | STAGE IV SPORULATION PROTEIN. |
| | ID3429 | S | BH2350 PROTEIN. |
| | ID3430 | S | DNA, COMPLETE SEQUENCE. |
| | ID3431 | S | ORF10. |
| | ID3432 | S | ORF starting with ATG of length 700 |
| 35 | ID3433 | S | ORF starting with ATG of length 801 |
| | ID3434 | S | BH4025 PROTEIN. |
| | ID3435 | S | UNKNOWN PROTEIN. |
| | ID3436 | S | HYPOTHETICAL 46.1 KDA PROTEIN IN PLSC 3'REGION. |
| | ID3437 | S | BH2390 PROTEIN. |
| 40 | ID3438 | S | BH2389 PROTEIN. |
| | ID3439 | S | ORF starting with ATG of length 426 |
| | ID3440 | S | TRANSPOSSASE (22). |
| | ID3441 | S | ORF starting with ATG of length 588 |
| | ID3442 | S | LPLC PROTEIN. |
| 45 | ID3443 | S | ORF starting with ATG of length 2421 |
| | ID3444 | S | BH0970 PROTEIN. |
| | ID3445 | S | CHORISMATE MUTASE (ISOZYMES 1 AND 2). |
| | ID3446 | S | ORF starting with ATG of length 525 |
| | ID3447 | S | ORF starting with ATG of length 486 |
| 50 | ID3448 | S | ORF starting with ATG of length 609 |
| | ID3449 | S | HYPOTHETICAL 30.7 KDA PROTEIN. |
| | ID3450 | S | Human gene 8 encoded secreted protein HMAM121, SEQ ID NO:137 |
| | ID3451 | S | BH1071 PROTEIN. |
| 55 | ID3452 | S | BH1089 PROTEIN. |
| | ID3453 | S | ORF starting with ATG of length 363 |
| | ID3454 | S | Staphylococcus aureus protein homologous to subunit fmdE. |
| | ID3455 | S | MAGNESIUM CITRATE SECONDARY TRANSPORTER. |
| 60 | ID3456 | S | BH0709 PROTEIN. |
| | ID3457 | S | UNKNOWN PROTEIN. |
| | ID3458 | S | ORF starting with ATG of length 483 |
| | ID3459 | S | YJDC PROTEIN. |
| | ID3460 | S | BH2596 PROTEIN. |
| 65 | ID3461 | S | BH2622 PROTEIN. |
| | ID3462 | S | ORF starting with ATG of length 662 |

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| | ID3463 | S | BH0236 PROTEIN. |
| | ID3464 | S | BH2637 PROTEIN. |
| | ID3465 | S | BH2638 PROTEIN. |
| | ID3466 | S | BH0424 PROTEIN. |
| 5 | ID3467 | S | SUGAR TRANSPORT SYSTEM (PERMEASE). |
| | ID3468 | S | ENOYL- [ACYL-CARRIER PROTEIN] REDUCTASE. |
| | ID3469 | S | BH2840 PROTEIN. |
| | ID3470 | S | ORF starting with ATG of length 807 |
| | ID3471 | S | BH2838 PROTEIN. |
| 10 | ID3472 | S | BH2837 PROTEIN. |
| | ID3473 | S | GERMINATION (CORTEX HYDROLYSIS) AND SPORULATION |
| | (STAGE II, M | | |
| | ID3474 | S | REGULATORY PROTEIN. |
| 15 | ID3475 | S | PUTATIVE GLYCOSYLTRANSFERASE CPSIVM. |
| | ID3476 | S | INNER SPORE COAT PROTEIN D. |
| | ID3477 | S | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3478 | S | YETF PROTEIN. |
| | ID3479 | S | SMALL, ACID-SOLUBLE SPORE PROTEIN D (SASP). |
| | ID3480 | S | Cyclohexanone monooxygenase sequence. |
| 20 | ID3481 | S | KIAA1655 PROTEIN (FRAGMENT). |
| | ID3482 | S | RIBONUCLEASE HII (EC 3.1.26.4) (RNASE HII) |
| | (FRAGMENT). | | |
| | ID3483 | S | CAPSID PROTEIN (F PROTEIN) (GPF). |
| | ID3484 | S | BH1804 PROTEIN. |
| 25 | ID3485 | S | ORF starting with ATG of length 288 |
| | ID3486 | S | ORF starting with ATG of length 417 |
| | ID3487 | S | ORF starting with ATG of length 469 |
| | ID3488 | S | BH3433 PROTEIN. |
| | ID3489 | S | BH3337 PROTEIN. |
| 30 | ID3490 | S | BH3430 PROTEIN. |
| | ID3491 | S | ORF starting with ATG of length 809 |
| | ID3492 | S | ORF starting with ATG of length 1188 |
| | ID3493 | S | HYPOTHETICAL 15.7 KDA PROTEIN IN PBPD-COMA INTERGENIC |
| | REGION | | |
| 35 | ID3494 | S | BH2622 PROTEIN. |
| | ID3495 | S | ORF15. |
| | ID3496 | S | TRANSCRIPTIONAL REGULATOR (LYSR FAMILY). |
| | ID3497 | S | ORF starting with ATG of length 478 |
| | ID3498 | S | ORF starting with ATG of length 526 |
| 40 | ID3499 | S | TRANSPOSSASE (22). |
| | ID3500 | S | Chlamydia pneumoniae lipoprotein sequence. |
| | ID3501 | S | BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE E2. |
| | ID3502 | S | BH1247 PROTEIN. |
| | ID3503 | S | ORF starting with ATG of length 696 |
| 45 | ID3504 | S | ORF starting with ATG of length 384 |
| | ID3505 | S | ORF starting with ATG of length 621 |
| | ID3506 | S | HYPOTHETICAL 25.4 KDA PROTEIN IN DPPE-HMP INTERGENIC |
| | REGION | | |
| 50 | ID3507 | S | ORF starting with ATG of length 226 |
| | ID3508 | S | ORF starting with ATG of length 233 |
| | ID3509 | S | ORF starting with ATG of length 216 |
| | ID3510 | S | ORF starting with ATG of length 396 |
| | ID3511 | S | ORF starting with ATG of length 441 |
| | ID3512 | S | ORF starting with ATG of length 298 |
| 55 | ID3513 | S | ORF starting with ATG of length 273 |
| | ID3514 | S | ORF starting with ATG of length 339 |
| | ID3515 | S | ORF starting with ATG of length 213 |
| | ID3516 | S | ORF starting with ATG of length 271 |
| | ID3517 | S | ORF starting with ATG of length 384 |
| 60 | ID3518 | S | ORF starting with ATG of length 267 |
| | ID3519 | S | ORF starting with ATG of length 240 |
| | ID3520 | S | ORF starting with ATG of length 249 |
| | ID3521 | S | ORF starting with ATG of length 231 |
| | ID3522 | S | ORF starting with ATG of length 270 |
| 65 | ID3523 | S | ORF starting with ATG of length 437 |
| | ID3524 | S | ORF starting with ATG of length 474 |

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|----|--------|---|--------------------------------------------|
| | ID3525 | S | ORF starting with ATG of length 309 |
| | ID3526 | S | ORF starting with ATG of length 273 |
| | ID3527 | S | ORF starting with ATG of length 246 |
| | ID3528 | S | ORF starting with ATG of length 543 |
| 5 | ID3529 | S | ORF starting with ATG of length 318 |
| | ID3530 | S | ORF starting with ATG of length 249 |
| | ID3531 | S | ORF starting with ATG of length 213 |
| | ID3532 | S | ORF starting with ATG of length 260 |
| | ID3533 | S | ORF starting with ATG of length 203 |
| 10 | ID3534 | S | ORF starting with ATG of length 243 |
| | ID3535 | S | ORF starting with ATG of length 218 |
| | ID3536 | S | ORF starting with ATG of length 219 |
| | ID3537 | S | ORF starting with ATG of length 219 |
| | ID3538 | S | ORF starting with ATG of length 573 |
| 15 | ID3539 | S | ORF starting with ATG of length 648 |
| | ID3540 | S | ORF starting with ATG of length 204 |
| | ID3541 | S | ORF starting with ATG of length 351 |
| | ID3542 | S | ORF starting with ATG of length 387 |
| | ID3543 | S | ORF starting with ATG of length 267 |
| 20 | ID3544 | S | ORF starting with ATG of length 285 |
| | ID3545 | S | ORF starting with ATG of length 337 |
| | ID3546 | S | ORF starting with ATG of length 441 |
| | ID3547 | S | ORF starting with ATG of length 325 |
| | ID3548 | S | ORF starting with ATG of length 226 |
| 25 | ID3549 | S | ORF starting with ATG of length 437 |
| | ID3550 | S | ORF starting with ATG of length 288 |
| | ID3551 | S | ORF starting with ATG of length 306 |
| | ID3552 | S | ORF starting with ATG of length 549 |
| | ID3553 | S | ORF starting with ATG of length 375 |
| 30 | ID3554 | S | ORF starting with ATG of length 326 |
| | ID3555 | S | ORF starting with ATG of length 339 |
| | ID3556 | S | ORF starting with ATG of length 453 |
| | ID3557 | S | ORF starting with ATG of length 312 |
| | ID3558 | S | ORF starting with ATG of length 354 |
| 35 | ID3559 | S | ORF starting with ATG of length 225 |
| | ID3560 | S | ORF starting with ATG of length 370 |
| | ID3561 | S | ORF starting with ATG of length 273 |
| | ID3562 | S | ORF starting with ATG of length 281 |
| | ID3563 | S | ORF starting with ATG of length 240 |
| 40 | ID3564 | S | ORF starting with ATG of length 258 |
| | ID3565 | S | ORF starting with ATG of length 347 |
| | ID3566 | S | ORF starting with ATG of length 204 |
| | ID3567 | S | ORF starting with TTG or GTG of length 485 |
| | ID3568 | S | ORF starting with ATG of length 448 |
| 45 | ID3569 | S | ORF starting with ATG of length 249 |
| | ID3570 | S | ORF starting with ATG of length 366 |
| | ID3571 | S | ORF starting with ATG of length 302 |
| | ID3572 | S | ORF starting with TTG or GTG of length 408 |
| | ID3573 | S | ORF starting with ATG of length 240 |
| 50 | ID3574 | S | ORF starting with ATG of length 273 |
| | ID3575 | S | ORF starting with ATG of length 249 |
| | ID3576 | S | ORF starting with ATG of length 468 |
| | ID3577 | S | ORF starting with ATG of length 339 |
| | ID3578 | S | ORF starting with ATG of length 209 |
| 55 | ID3579 | S | ORF starting with ATG of length 293 |
| | ID3580 | S | ORF starting with ATG of length 207 |
| | ID3581 | S | ORF starting with ATG of length 246 |
| | ID3582 | S | ORF starting with ATG of length 258 |
| | ID3583 | S | ORF starting with ATG of length 228 |
| 60 | ID3584 | S | ORF starting with ATG of length 213 |
| | ID3585 | S | ORF starting with ATG of length 204 |
| | ID3586 | S | ORF starting with ATG of length 345 |
| | ID3587 | S | ORF starting with ATG of length 561 |
| | ID3588 | S | ORF starting with ATG of length 201 |
| 65 | ID3589 | S | ORF starting with ATG of length 417 |
| | ID3590 | S | ORF starting with ATG of length 376 |

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| | ID3591 | S | ORF starting with ATG of length 294 |
| | ID3592 | S | ORF starting with TTG or GTG of length 408 |
| | ID3593 | S | ORF starting with ATG of length 279 |
| | ID3594 | S | ORF starting with ATG of length 427 |
| 5 | ID3595 | S | ORF starting with ATG of length 318 |
| | ID3596 | S | ORF starting with ATG of length 477 |
| | ID3597 | S | ORF starting with ATG of length 297 |
| | ID3598 | S | ORF starting with ATG of length 222 |
| | ID3599 | S | ORF starting with ATG of length 225 |
| 10 | ID3600 | S | ORF starting with ATG of length 270 |
| | ID3601 | S | ORF starting with ATG of length 435 |
| | ID3602 | S | ORF starting with ATG of length 474 |
| | ID3603 | S | ORF starting with ATG of length 525 |
| | ID3604 | S | ORF starting with TTG or GTG of length 510 |
| 15 | ID3605 | S | ORF starting with ATG of length 207 |
| | ID3606 | S | ORF starting with ATG of length 222 |
| | ID3607 | S | ORF starting with ATG of length 474 |
| | ID3608 | S | ORF starting with ATG of length 435 |
| 20 | ID3609 | S | ORF starting with ATG of length 261 |
| | ID3610 | S | ORF starting with ATG of length 287 |
| | ID3611 | S | ORF starting with ATG of length 288 |
| | ID3612 | S | ORF starting with ATG of length 212 |
| | ID3613 | S | ORF starting with ATG of length 282 |
| | ID3614 | S | ORF starting with ATG of length 241 |
| 25 | ID3615 | S | ORF starting with ATG of length 243 |
| | ID3616 | S | ORF starting with ATG of length 210 |
| | ID3617 | S | ORF starting with ATG of length 342 |
| | ID3618 | S | ORF starting with ATG of length 250 |
| 30 | ID3619 | S | ORF starting with ATG of length 233 |
| | ID3620 | S | ORF starting with ATG of length 272 |
| | ID3621 | S | ORF starting with ATG of length 558 |
| | ID3622 | S | ORF starting with ATG of length 290 |
| | ID3623 | S | ORF starting with ATG of length 413 |
| | ID3624 | S | ORF starting with ATG of length 213 |
| 35 | ID3625 | S | ORF starting with ATG of length 304 |
| | ID3626 | S | ORF starting with ATG of length 702 |
| | ID3627 | S | ORF starting with ATG of length 351 |
| | ID3628 | S | ORF starting with ATG of length 654 |
| | ID3629 | S | ORF starting with ATG of length 264 |
| 40 | ID3630 | S | ORF starting with ATG of length 264 |
| | ID3631 | S | ORF starting with ATG of length 591 |
| | ID3632 | S | ORF starting with ATG of length 318 |
| | ID3633 | S | ORF starting with ATG of length 268 |
| | ID3634 | S | ORF starting with ATG of length 525 |
| 45 | ID3635 | S | ORF starting with ATG of length 270 |
| | ID3636 | S | ORF starting with ATG of length 609 |
| | ID3637 | S | ORF starting with ATG of length 267 |
| | ID3638 | S | ORF starting with ATG of length 444 |
| | ID3639 | S | ORF starting with ATG of length 285 |
| 50 | ID3640 | S | ORF starting with ATG of length 307 |
| | ID3641 | S | ORF starting with ATG of length 306 |
| | ID3642 | S | ORF starting with ATG of length 397 |
| | ID3643 | S | ORF starting with ATG of length 220 |
| | ID3644 | S | ORF starting with ATG of length 249 |
| 55 | ID3645 | S | ORF starting with TTG or GTG of length 423 |
| | ID3646 | S | ORF starting with ATG of length 455 |
| | ID3647 | S | ORF starting with ATG of length 227 |
| | ID3648 | S | ORF starting with ATG of length 210 |
| | ID3649 | S | ORF starting with ATG of length 363 |
| 60 | ID3650 | S | ORF starting with ATG of length 366 |
| | ID3651 | S | ORF starting with ATG of length 273 |
| | ID3652 | S | ORF starting with ATG of length 306 |
| | ID3653 | S | ORF starting with TTG or GTG of length 402 |
| | ID3654 | S | ORF starting with ATG of length 252 |
| 65 | ID3655 | S | ORF starting with ATG of length 231 |
| | ID3656 | S | ORF starting with ATG of length 327 |

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|----|--------|---|--------------------------------------------|
| | ID3657 | S | ORF starting with ATG of length 287 |
| | ID3658 | S | ORF starting with ATG of length 204 |
| | ID3659 | S | ORF starting with ATG of length 1423 |
| | ID3660 | S | ORF starting with ATG of length 309 |
| 5 | ID3661 | S | ORF starting with ATG of length 309 |
| | ID3662 | S | ORF starting with ATG of length 525 |
| | ID3663 | S | ORF starting with ATG of length 225 |
| | ID3664 | S | ORF starting with ATG of length 360 |
| | ID3665 | S | ORF starting with ATG of length 272 |
| 10 | ID3666 | S | ORF starting with ATG of length 201 |
| | ID3667 | S | ORF starting with ATG of length 339 |
| | ID3668 | S | ORF starting with ATG of length 483 |
| | ID3669 | S | ORF starting with ATG of length 384 |
| | ID3670 | S | ORF starting with ATG of length 225 |
| 15 | ID3671 | S | ORF starting with ATG of length 213 |
| | ID3672 | S | ORF starting with ATG of length 234 |
| | ID3673 | S | ORF starting with ATG of length 397 |
| | ID3674 | S | ORF starting with ATG of length 348 |
| | ID3675 | S | ORF starting with ATG of length 258 |
| 20 | ID3676 | S | ORF starting with ATG of length 471 |
| | ID3677 | S | ORF starting with ATG of length 213 |
| | ID3678 | S | ORF starting with ATG of length 285 |
| | ID3679 | S | ORF starting with ATG of length 272 |
| | ID3680 | S | ORF starting with ATG of length 357 |
| 25 | ID3681 | S | ORF starting with TTG or GTG of length 435 |
| | ID3682 | S | ORF starting with ATG of length 729 |
| | ID3683 | S | ORF starting with ATG of length 909 |
| | ID3684 | S | ORF starting with ATG of length 276 |
| | ID3685 | S | ORF starting with ATG of length 270 |
| 30 | ID3686 | S | ORF starting with ATG of length 330 |
| | ID3687 | S | ORF starting with ATG of length 310 |
| | ID3688 | S | ORF starting with ATG of length 300 |
| | ID3689 | S | ORF starting with ATG of length 615 |
| | ID3690 | S | ORF starting with ATG of length 381 |
| 35 | ID3691 | S | ORF starting with ATG of length 291 |
| | ID3692 | S | ORF starting with ATG of length 207 |
| | ID3693 | S | ORF starting with ATG of length 201 |
| | ID3694 | S | ORF starting with ATG of length 801 |
| | ID3695 | S | ORF starting with ATG of length 501 |
| 40 | ID3696 | S | ORF starting with ATG of length 474 |
| | ID3697 | S | ORF starting with ATG of length 255 |
| | ID3698 | S | ORF starting with ATG of length 300 |
| | ID3699 | S | ORF starting with TTG or GTG of length 558 |
| | ID3700 | S | ORF starting with ATG of length 204 |
| 45 | ID3701 | S | ORF starting with ATG of length 222 |
| | ID3702 | S | ORF starting with ATG of length 276 |
| | ID3703 | S | ORF starting with ATG of length 559 |
| | ID3704 | S | ORF starting with ATG of length 220 |
| | ID3705 | S | ORF starting with ATG of length 213 |
| 50 | ID3706 | S | ORF starting with ATG of length 375 |
| | ID3707 | S | ORF starting with ATG of length 255 |
| | ID3708 | S | ORF starting with TTG or GTG of length 435 |
| | ID3709 | S | ORF starting with ATG of length 621 |
| | ID3710 | S | ORF starting with ATG of length 270 |
| 55 | ID3711 | S | ORF starting with ATG of length 204 |
| | ID3712 | S | ORF starting with ATG of length 207 |
| | ID3713 | S | ORF starting with ATG of length 204 |
| | ID3714 | S | ORF starting with ATG of length 309 |
| | ID3715 | S | ORF starting with ATG of length 243 |
| 60 | ID3716 | S | ORF starting with ATG of length 819 |
| | ID3717 | S | ORF starting with ATG of length 213 |
| | ID3718 | S | ORF starting with ATG of length 364 |
| | ID3719 | S | ORF starting with ATG of length 345 |
| | ID3720 | S | ORF starting with ATG of length 207 |
| 65 | ID3721 | S | ORF starting with ATG of length 486 |
| | ID3722 | S | ORF starting with ATG of length 351 |

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|----|--------|---|--------------------------------------------|
| | ID3723 | S | ORF starting with ATG of length 213 |
| | ID3724 | S | ORF starting with ATG of length 663 |
| | ID3725 | S | ORF starting with ATG of length 525 |
| | ID3726 | S | ORF starting with ATG of length 228 |
| 5 | ID3727 | S | ORF starting with ATG of length 207 |
| | ID3728 | S | ORF starting with ATG of length 375 |
| | ID3729 | S | ORF starting with ATG of length 564 |
| | ID3730 | S | ORF starting with ATG of length 369 |
| | ID3731 | S | ORF starting with ATG of length 230 |
| 10 | ID3732 | S | ORF starting with ATG of length 226 |
| | ID3733 | S | ORF starting with ATG of length 654 |
| | ID3734 | S | ORF starting with ATG of length 463 |
| | ID3735 | S | ORF starting with ATG of length 444 |
| | ID3736 | S | ORF starting with ATG of length 375 |
| 15 | ID3737 | S | ORF starting with ATG of length 209 |
| | ID3738 | S | ORF starting with ATG of length 236 |
| | ID3739 | S | ORF starting with ATG of length 349 |
| | ID3740 | S | ORF starting with ATG of length 210 |
| 20 | ID3741 | S | ORF starting with ATG of length 215 |
| | ID3742 | S | ORF starting with ATG of length 267 |
| | ID3743 | S | ORF starting with ATG of length 220 |
| | ID3744 | S | ORF starting with TTG or GTG of length 411 |
| | ID3745 | S | ORF starting with ATG of length 231 |
| | ID3746 | S | ORF starting with ATG of length 336 |
| 25 | ID3747 | S | ORF starting with ATG of length 320 |
| | ID3748 | S | ORF starting with ATG of length 492 |
| | ID3749 | S | ORF starting with ATG of length 358 |
| | ID3750 | S | ORF starting with ATG of length 270 |
| 30 | ID3751 | S | ORF starting with ATG of length 441 |
| | ID3752 | S | ORF starting with ATG of length 279 |
| | ID3753 | S | ORF starting with ATG of length 493 |
| | ID3754 | S | ORF starting with ATG of length 273 |
| | ID3755 | S | ORF starting with ATG of length 384 |
| | ID3756 | S | ORF starting with ATG of length 577 |
| 35 | ID3757 | S | ORF starting with ATG of length 216 |
| | ID3758 | S | ORF starting with ATG of length 278 |
| | ID3759 | S | ORF starting with TTG or GTG of length 612 |
| | ID3760 | S | ORF starting with TTG or GTG of length 432 |
| | ID3761 | S | ORF starting with ATG of length 605 |
| 40 | ID3762 | S | ORF starting with ATG of length 243 |
| | ID3763 | S | ORF starting with ATG of length 363 |
| | ID3764 | S | ORF starting with ATG of length 606 |
| | ID3765 | S | ORF starting with ATG of length 376 |
| | ID3766 | S | ORF starting with ATG of length 279 |
| 45 | ID3767 | S | ORF starting with ATG of length 318 |
| | ID3768 | S | ORF starting with ATG of length 294 |
| | ID3769 | S | ORF starting with ATG of length 557 |
| | ID3770 | S | ORF starting with ATG of length 256 |
| | ID3771 | S | ORF starting with ATG of length 253 |
| 50 | ID3772 | S | ORF starting with ATG of length 408 |
| | ID3773 | S | ORF starting with ATG of length 599 |
| | ID3774 | S | ORF starting with ATG of length 259 |
| | ID3775 | S | ORF starting with TTG or GTG of length 627 |
| | ID3776 | S | ORF starting with ATG of length 492 |
| 55 | ID3777 | S | ORF starting with ATG of length 376 |
| | ID3778 | S | ORF starting with ATG of length 300 |
| | ID3779 | S | ORF starting with ATG of length 204 |
| | ID3780 | S | ORF starting with ATG of length 1002 |
| | ID3781 | S | ORF starting with ATG of length 325 |
| 60 | ID3782 | S | ORF starting with ATG of length 255 |
| | ID3783 | S | ORF starting with TTG or GTG of length 633 |
| | ID3784 | S | ORF starting with ATG of length 309 |
| | ID3785 | S | ORF starting with ATG of length 276 |
| | ID3786 | S | ORF starting with ATG of length 559 |
| 65 | ID3787 | S | ORF starting with ATG of length 231 |
| | ID3788 | S | ORF starting with ATG of length 219 |

| | | | |
|----|--------|---|--------------------------------------------------------------|
| | ID3789 | S | ORF starting with ATG of length 216 |
| | ID3790 | S | ORF starting with ATG of length 681 |
| | ID3791 | S | ORF starting with ATG of length 345 |
| 5 | ID3792 | S | ORF starting with ATG of length 301 |
| | ID3793 | S | ORF starting with ATG of length 202 |
| | ID3794 | S | ORF starting with ATG of length 576 |
| | ID3795 | S | ORF starting with ATG of length 327 |
| | ID3796 | S | ORF starting with ATG of length 461 |
| | ID3797 | S | ORF starting with ATG of length 231 |
| 10 | ID3798 | S | ORF starting with ATG of length 765 |
| | ID3799 | S | ORF starting with ATG of length 210 |
| | ID3800 | S | ORF starting with ATG of length 222 |
| | ID3801 | S | ORF starting with ATG of length 300 |
| | ID3802 | S | ORF starting with ATG of length 322 |
| 15 | ID3803 | S | ORF starting with ATG of length 213 |
| | ID3804 | S | ORF starting with ATG of length 798 |
| | ID3805 | S | ORF starting with ATG of length 537 |
| | ID3806 | S | ORF starting with ATG of length 258 |
| | ID3807 | S | ORF starting with ATG of length 216 |
| 20 | ID3808 | S | ORF starting with ATG of length 224 |
| | ID3809 | S | ORF starting with ATG of length 426 |
| | ID3810 | S | ORF starting with ATG of length 339 |
| | ID3811 | S | ORF starting with ATG of length 218 |
| | ID3812 | S | ORF starting with ATG of length 495 |
| 25 | ID3813 | S | ORF starting with ATG of length 309 |
| | ID3814 | S | ORF starting with ATG of length 225 |
| | ID3815 | S | ORF starting with ATG of length 210 |
| | ID3816 | S | ORF starting with ATG of length 954 |
| | ID3817 | S | ORF starting with ATG of length 243 |
| 30 | ID3818 | S | ORF starting with ATG of length 336 |
| | ID3819 | S | ORF starting with ATG of length 388 |
| | ID3820 | S | ORF starting with ATG of length 335 |
| | ID3821 | S | ORF starting with ATG of length 226 |
| | ID3822 | S | ORF starting with ATG of length 279 |
| 35 | ID3823 | S | ORF starting with ATG of length 237 |
| | ID3824 | S | ORF starting with ATG of length 339 |
| | ID3825 | S | ORF starting with ATG of length 447 |
| | ID3826 | S | ORF starting with ATG of length 246 |
| | ID3827 | S | ORF starting with ATG of length 366 |
| 40 | ID3828 | S | ORF starting with ATG of length 266 |
| | ID3829 | S | ORF starting with ATG of length 243 |
| | ID3830 | S | ORF starting with ATG of length 954 |
| | ID3831 | S | ORF starting with ATG of length 270 |
| | ID3832 | S | ORF starting with ATG of length 306 |
| 45 | ID3833 | S | ORF starting with ATG of length 366 |
| | ID3834 | S | ORF starting with ATG of length 204 |
| | ID3835 | S | ORF starting with ATG of length 342 |
| | ID3836 | S | ORF starting with ATG of length 339 |
| | ID3837 | S | ORF starting with ATG of length 243 |
| 50 | ID3838 | S | ORF starting with ATG of length 360 |
| | ID3839 | S | ORF starting with ATG of length 301 |
| | ID3840 | S | ORF starting with ATG of length 228 |
| | ID3841 | S | ORF starting with ATG of length 465 |
| | ID3842 | S | ORF starting with ATG of length 1182 |
| 55 | ID3843 | S | ORF starting with ATG of length 516 |
| | ID3844 | S | ORF starting with ATG of length 204 |
| | ID3845 | S | ORF starting with ATG of length 1000 |
| | ID3846 | S | ORF starting with ATG of length 207 |
| | ID3847 | S | ORF starting with ATG of length 285 |
| 60 | ID3848 | S | ORF starting with ATG of length 339 |
| | ID3849 | S | ORF starting with ATG of length 447 |
| | ID3850 | S | ORF starting with ATG of length 282 |
| | ID3851 | S | ORF starting with ATG of length 819 |
| | ID3852 | T | PUTATIVE SIGMA-B REGULATOR. |
| 65 | ID3853 | T | NEGATIVE REGULATOR OF SIGMA-B ACTIVITY (ANTAGONIST OF RSBT). |

| | | | |
|----|--------|---|----------------------------------------------------------------|
| | ID3854 | T | POSITIVE REGULATOR OF SIGMA-B ACTIVITY (SWITCH PROTEIN/SERIN). |
| | ID3855 | T | ANTI-SIGMA F FACTOR (STAGE II SPORULATION PROTEIN AB). |
| 5 | ID3856 | T | ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN). |
| | ID3857 | T | GENERAL STRESS PROTEIN 160 (GSP160). |
| | ID3858 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE INVOLVED IN DEGRADATION. |
| 10 | ID3859 | T | TRANSCRIPTIONAL REGULATOR. |
| | ID3860 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE INVOLVED IN PHOSPHATASE. |
| | ID3861 | T | SERINE PROTEIN KINASE. |
| | ID3862 | T | SERINE/THREONINE-PROTEIN KINASE. |
| 15 | ID3863 | T | ARSENATE REDUCTASE (EC 1.). |
| | ID3864 | T | CONSERVED HYPOTHETICAL PROTEIN. |
| | ID3865 | T | CARBON STARVATION PROTEIN A HOMOLOG. |
| | ID3866 | T | POLAR FLAGELLAR PROTEIN. |
| 20 | ID3867 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3868 | T | CARBON STARVATION PROTEIN A HOMOLOG. |
| | ID3869 | T | CITS (TWO-COMPONENT SENSOR HISTIDINE KINASE). |
| | ID3870 | T | KIN1 PROTEIN (PUTATIVE SENSORY TRANSDUCTION HISTIDINE KINASE). |
| | ID3871 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| 25 | ID3872 | T | BH0289 PROTEIN. |
| | ID3873 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3874 | T | ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER). |
| | ID3875 | T | BH1859 PROTEIN. |
| 30 | ID3876 | T | TWO-COMPONENT RESPONSE REGULATOR INVOLVED IN MODULATION OF F. |
| | ID3877 | T | ORF starting with ATG of length 709 |
| | ID3878 | T | TRANSCRIPTIONAL REGULATOR. |
| | ID3879 | T | ORF starting with ATG of length 1347 |
| | ID3880 | T | PUTATIVE INTEGRAL MEMBRANE PROTEIN (CSTA-LIKE). |
| 35 | ID3881 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3882 | T | CHEMOTAXIS CHEV PROTEIN (EC 2.7.3.-). |
| | ID3883 | T | SUBTILIN BIOSYNTHESIS SENSOR PROTEIN SPAK (EC 2.7.3.-). |
| | ID3884 | T | NEGATIVE REGULATOR OF SIGMA-B ACTIVITY (SWITCH PROTEIN/SERIN). |
| 40 | ID3885 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3886 | T | BH3353 PROTEIN. |
| | ID3887 | T | SERINE PROTEIN KINASE. |
| | ID3888 | T | BH2734 PROTEIN. |
| 45 | ID3889 | T | BH3833 PROTEIN. |
| | ID3890 | T | VPSR. |
| | ID3891 | T | NTRB, NTRC. |
| | ID3892 | T | ORF starting with ATG of length 1557 |
| | ID3893 | T | YVQE PROTEIN. |
| 50 | ID3894 | T | HYPOTHETICAL 40.2 KDA PROTEIN. |
| | ID3895 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3896 | T | TRANSCRIPTIONAL REGULATOR. |
| | ID3897 | T | SERINE PROTEIN KINASE. |
| | ID3898 | T | HYPOTHETICAL 58.9 KDA PROTEIN. |
| 55 | ID3899 | T | NEGATIVE REGULATOR OF SIGMA-B ACTIVITY (SWITCH PROTEIN/SERIN). |
| | ID3900 | T | YLAK PROTEIN. |
| | ID3901 | T | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3902 | T | YTAB PROTEIN. |
| 60 | ID3903 | T | SERINE/THREONINE PROTEIN KINASE. |
| | ID3904 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3905 | T | CARBON STARVATION PROTEIN A, PUTATIVE. |
| | ID3906 | T | AUTOLYSIN RESPONSE REGULATOR. |
| | ID3907 | T | BH3353 PROTEIN. |
| 65 | ID3908 | T | YLOO PROTEIN. |
| | ID3909 | T | YTAB PROTEIN. |

| | | | |
|----|-----------------|----|---------------------------------------------------------------|
| | ID3910 | T | KIN1 PROTEIN (PUTATIVE SENSORY TRANSDUCTION HISTIDINE KINASE) |
| | ID3911 | T | ORF4 PROTEIN. |
| | ID3912 | T | BH2734 PROTEIN. |
| 5 | ID3913 | T | TWO-COMPONENT SENSOR HISTIDINE KINASE. |
| | ID3914 | T | SUBTILIN BIOSYNTHESIS SENSOR PROTEIN SPAK (EC 2.7.3.-). |
| | ID3915 | TK | PUTATIVE TWO-COMPONENT RESPONSE REGULATOR. |
| 10 | ID3916 | TK | GTP PYROPHOSPHOKINASE (STRINGENT RESPONSE). |
| | ID3917 | TK | TWO-COMPONENT RESPONSE REGULATOR INVOLVED IN |
| | PHOSPHATE REGUL | | TRANSCRIPTIONAL REGULATORY PROTEIN DEGU. |
| | ID3918 | TK | STAGE II SPORULATION PROTEIN E. |
| | ID3919 | TK | Mycobacterium bovis regX3 protein. |
| 15 | ID3920 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3921 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3922 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3923 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3924 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| 20 | ID3925 | TK | STAGE II SPORULATION PROTEIN E. |
| | ID3926 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3927 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3928 | TK | SUBTILIN BIOSYNTHESIS REGULATORY PROTEIN SPAR. |
| | ID3929 | TK | INDIRECT POSITIVE REGULATOR OF SIGMA-B ACTIVITY |
| | (SERINE PHOS | | |
| 25 | ID3930 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3931 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3932 | TK | TWO-COMPONENT RESPONSE REGULATOR. |
| | ID3933 | TK | PUTATIVE RESPONSE REGULATOR. |
| | ID3934 | TK | STAGE II SPORULATION PROTEIN E. |
| 30 | ID3935 | TK | Staphylococcus aureus protein SEQ ID #5239. |
| | ID3936 | TK | GTP PYROPHOSPHOKINASE (STRINGENT RESPONSE). |
| | ID3937 | TQ | ORF starting with ATG of length 453 |
| | ID3938 | TQ | ORF starting with ATG of length 636 |
| | ID3939 | TQ | YUK[A,B,C,D,E,F], YUK[I,J,K,L,M] AND ALD GENES. |
| 35 | ID3940 | TQ | BH2731 PROTEIN. |
| | ID3941 | TQ | BH1735 PROTEIN. |
| | ID3942 | TQ | BH0757 PROTEIN. |
| | ID3943 | TQ | ORF starting with ATG of length 975 |
| | ID3944 | TQ | YUK[A,B,C,D,E,F], YUK[I,J,K,L,M] AND ALD GENES. |
| 40 | ID3945 | TQ | ORF starting with ATG of length 513 |
| | ID3946 | TQ | ACETOIN DEHYDROGENASE. |
| | ID3947 | TQ | BH1735 PROTEIN. |
| | ID3948 | Z | transfer RNA-Ala |
| | ID3949 | Z | transfer RNA-Ile |
| 45 | ID3950 | Z | transfer RNA-Ala |
| | ID3951 | Z | transfer RNA-Arg |
| | ID3952 | Z | transfer RNA-Asn |
| | ID3953 | Z | transfer RNA-Asp |
| | ID3954 | Z | transfer RNA-Glu |
| 50 | ID3955 | Z | transfer RNA-Gly |
| | ID3956 | Z | transfer RNA-Gly |
| | ID3957 | Z | transfer RNA-His |
| | ID3958 | Z | transfer RNA-Ile |
| | ID3959 | Z | transfer RNA-Leu |
| 55 | ID3960 | Z | transfer RNA-Leu |
| | ID3961 | Z | transfer RNA-Lys |
| | ID3962 | Z | transfer RNA-Met |
| | ID3963 | Z | transfer RNA-Met |
| | ID3964 | Z | transfer RNA-Met |
| 60 | ID3965 | Z | transfer RNA-Phe |
| | ID3966 | Z | transfer RNA-Pro |
| | ID3967 | Z | transfer RNA-Ser |
| | ID3968 | Z | transfer RNA-Ser |
| | ID3969 | Z | transfer RNA-Thr |
| 65 | ID3970 | Z | transfer RNA-Val |
| | ID3971 | Z | transfer RNA-Asn |

| | | | |
|----|--------|---|-------------------|
| | ID3972 | Z | transfer RNA-Asp |
| | ID3973 | Z | transfer RNA-Cys |
| | ID3974 | Z | transfer RNA-Gln |
| | ID3975 | Z | transfer RNA-Glu |
| 5 | ID3976 | Z | transfer RNA-Gly |
| | ID3977 | Z | transfer RNA-His |
| | ID3978 | Z | transfer RNA-Leu |
| | ID3979 | Z | transfer RNA-Leu |
| | ID3980 | Z | transfer RNA-Met |
| 10 | ID3981 | Z | transfer RNA-Phe |
| | ID3982 | Z | transfer RNA-Ser |
| | ID3983 | Z | transfer RNA-Thr |
| | ID3984 | Z | transfer RNA-Trp |
| | ID3985 | Z | transfer RNA-Val |
| 15 | ID3986 | Z | transfer RNA-Arg |
| | ID3987 | Z | transfer RNA-Asp |
| | ID3988 | Z | transfer RNA-Gly |
| | ID3989 | Z | transfer RNA-Met |
| 20 | ID3990 | Z | transfer RNA-Ala |
| | ID3991 | Z | transfer RNA-Arg |
| | ID3992 | Z | transfer RNA-Asn |
| | ID3993 | Z | transfer RNA-Gly |
| | ID3994 | Z | transfer RNA-Pro |
| | ID3995 | Z | transfer RNA-Thr |
| 25 | ID3996 | Z | transfer RNA-Ala |
| | ID3997 | Z | transfer RNA-Arg |
| | ID3998 | Z | transfer RNA-Gly |
| | ID3999 | Z | transfer RNA-Leu |
| 30 | ID4000 | Z | transfer RNA-Leu |
| | ID4001 | Z | transfer RNA-Lys |
| | ID4002 | Z | transfer RNA-Pro |
| | ID4003 | Z | transfer RNA-Thr |
| | ID4004 | Z | transfer RNA-Val |
| | ID4005 | Z | transfer RNA-Ala |
| 35 | ID4006 | Z | transfer RNA-Ile |
| | ID4007 | Z | transfer RNA-Arg |
| | ID4008 | Z | transfer RNA-Asn |
| | ID4009 | Z | transfer RNA-Gln |
| | ID4010 | Z | transfer RNA-Glu |
| 40 | ID4011 | Z | transfer RNA-Leu |
| | ID4012 | Z | transfer RNA-Leu |
| | ID4013 | Z | transfer RNA-Lys |
| | ID4014 | Z | transfer RNA-Ser |
| | ID4015 | Z | transfer RNA-Ala |
| 45 | ID4016 | Z | transfer RNA-Arg |
| | ID4017 | Z | transfer RNA-Gln |
| | ID4018 | Z | transfer RNA-Gln |
| | ID4019 | Z | transfer RNA-Glu |
| | ID4020 | Z | transfer RNA-Glu |
| 50 | ID4021 | Z | transfer RNA-Gly |
| | ID4022 | Z | transfer RNA-Met |
| | ID4023 | Z | transfer RNA-Ser |
| | ID4024 | Z | transfer RNA-Thr |
| | ID4025 | Z | transfer RNA-Val |
| 55 | ID4026 | Z | transfer RNA-Val |
| | ID4027 | Z | transfer RNA-Asp |
| | ID4028 | Z | transfer RNA-Glu |
| | ID4029 | Z | transfer RNA-Lys |
| | ID4030 | Z | transfer RNA-Phe |
| 60 | ID4031 | Z | ribosomal RNA-16S |
| | ID4032 | Z | ribosomal RNA-23S |
| | ID4033 | Z | ribosomal RNA-5S |

Claims**What is claimed is:**

5 1. A method for monitoring differential expression of a plurality of genes in a first *Bacillus* cell relative to expression of the same genes in one or more second *Bacillus* cells, comprising:

10 (a) adding a mixture of labeled nucleic acid probes isolated from the *Bacillus* cells to a substrate containing an array of *Bacillus* GSTs under conditions where the nucleic acids hybridize to complementary sequences of the *Bacillus* GSTs in the array, wherein the nucleic acids from the first *Bacillus* cell and the one or more second *Bacillus* cells are labeled with a first reporter and one or more different second reporters, respectively; and

15 (b) examining the array under conditions wherein the relative expression of the genes in the *Bacillus* cells is determined by the observed hybridization reporter signal of each spot in the array in which (i) the *Bacillus* GSTs in the array that hybridize to the nucleic acids obtained from either the first or the one or more second *Bacillus* cells produce a distinct first hybridization reporter signal or one or more second hybridization reporter signals, respectively, and (ii) the *Bacillus* GSTs in the array that hybridize to the nucleic acids obtained from both the first and one or more second *Bacillus* cells produce a distinct combined hybridization reporter signal.

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25 2. The method of claim 1, wherein the *Bacillus* GSTs are selected from the group consisting of *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus laetus*, *Bacillus lenthus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* GSTs.

30 3. The method of claim 1, wherein the *Bacillus* GSTs are *Bacillus licheniformis* GSTs.

4. The method of claim 3, wherein the *Bacillus licheniformis* GSTs are selected from the group consisting of SEQ ID NOs. 1-4448, nucleic acid fragments of SEQ ID NOs. 1-4448, and nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

5

5. The method of claim 3, wherein the *Bacillus licheniformis* GSTs are SEQ ID NOs. 1-4448.

6. The method of claim 3, wherein the *Bacillus licheniformis* GSTs are nucleic acid fragments of SEQ ID NOs. 1-4448.

10 7. The method of claim 3, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

15 8. The method of claim 7, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-4448.

9. The method of claim 8, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 1-4448.

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10. The method of claim 1, wherein the *Bacillus* GSTs are *Bacillus clausii* GSTs.

11. The method of claim 10, wherein the *Bacillus clausii* GSTs are selected from the group consisting of SEQ ID NOs. 4449-8481, nucleic acid fragments of SEQ ID NOs. 4449-8481, and nucleic acid sequences having at least 85% homology to SEQ ID NOs. 4449-8481.

25 12. The method of claim 10, wherein the *Bacillus clausii* GSTs are SEQ ID NOs. 4449-8481.

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13. The method of claim 10, wherein the *Bacillus clausii* GSTs are nucleic acid fragments of SEQ ID NOs. 4449-8481.

14. The method of claim 10, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 85% homology to SEQ ID NOs. 4449-8481.

5 15. The method of claim 14, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4449-8481.

16. The method of claim 15, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 4449-8481.

10 17. The method of any of claims 1-16, wherein the *Bacillus* cells are selected from the group consisting of a *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentinus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*,
15 *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* cell.

18. The method of any of claims 1-17, wherein the *Bacillus* cells are the same cell.

19. The method of any of claims 1-17, wherein the first *Bacillus* cell is a *Bacillus*
20 *licheniformis* or *Bacillus clausii* cell.

20. The method of claim 19, wherein the *Bacillus licheniformis* cells are *Bacillus licheniformis* ATCC 14580 cells.

25 21. The method of claim 19, wherein the *Bacillus clausii* cells are *Bacillus clausii* NCIB 10309 cells.

22. The method of any of claims 1-17, wherein the one or more second *Bacillus* cells are *Bacillus licheniformis* or *Bacillus clausii* cells.

30 23. The method of claim 22, wherein the *Bacillus licheniformis* cells are *Bacillus licheniformis* ATCC 14580 cells.

24. The method of claim 22, wherein the *Bacillus clausii* cells are *Bacillus clausii* NCIB 10309 cells.

5 25. The method of any of claims 1-17, wherein the *Bacillus* cells are one or more different cells.

26. The method of any of claims 1-25, wherein the hybridization conditions are selected from the group consisting of very low, low, low-medium, medium, medium-high, high, and very high stringency conditions.

10 27. The method of any of claims 1-26, wherein the reporters are colorimetric, radioactive, or fluorescent reporters.

15 28. A computer readable medium having recorded thereon an array of *Bacillus* GSTs.

29. The computer readable medium of claim 28, wherein the *Bacillus* GSTs are selected from the group consisting of *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*,
20 *Bacillus laetus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* GSTs.

30. The computer readable medium of claim 28, wherein the *Bacillus* GSTs are *Bacillus licheniformis* GSTs.

25 31. The computer readable medium of claim 30, wherein the *Bacillus licheniformis* GSTs are selected from the group consisting of SEQ ID NOs. 1-4448, nucleic acid fragments of SEQ ID NOs. 1-4448, and nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

30 32. The computer readable medium of claim 30, wherein the *Bacillus licheniformis* GSTs are SEQ ID NOs. 1-4448.

33. The computer readable medium of claim 30, wherein the *Bacillus licheniformis* GSTs are nucleic acid fragments of SEQ ID NOs. 1-4448.

5 34. The computer readable medium of claim 30, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

35. The computer readable medium of claim 34, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-4448.

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36. The computer readable medium of claim 35, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 1-4448.

15

37. The computer readable medium of claim 28, wherein the *Bacillus* GSTs are *Bacillus clausii* GSTs.

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38. The computer readable medium of claim 37, wherein the *Bacillus clausii* GSTs are selected from the group consisting of SEQ ID NOs. 4449-8481, nucleic acid fragments of SEQ ID NOs. 4449-8481, and nucleic acid sequences having at least 85% homology to SEQ ID NOs. 4449-8481.

39. The computer readable medium of claim 37, wherein the *Bacillus clausii* GSTs are SEQ ID NOs. 4449-8481.

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40. The computer readable medium of claim 37, wherein the *Bacillus clausii* GSTs are nucleic acid fragments of SEQ ID NOs. 4449-8481.

41. The computer readable medium of claim 37, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 85% homology to SEQ ID NOs. 4449-8481.

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42. The computer readable medium of claim 41, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4449-8481.

43. The computer readable medium of claim 42, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 4449-8481.

5) 44. The computer readable medium of any of claims 28-43, wherein the medium is selected from the group consisting of a floppy disk, a hard disk, random access memory (RAM), read only memory (ROM), and CD-ROM.

45. A computer-based system for monitoring differential expression of a plurality of genes in a first *Bacillus* cell relative to expression of the same genes in one or more second *Bacillus* cells comprising the following elements:

10 (a) a data storage means comprising *Bacillus* GSTs;
15 (b) a search means for comparing a target sequence to a *Bacillus* GST sequence of the data storage means of step (a) to identify homologous sequences; and

(c) a retrieval means for obtaining the homologous sequence(s) of step (b).

46. The computer-based system of claim 45, wherein the *Bacillus* GSTs are selected from the group consisting of *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus laetus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* GSTs.

47. The computer-based system of claim 45, wherein the *Bacillus* GSTs are *Bacillus licheniformis* GSTs.

48. The computer-based system of claim 47, wherein the *Bacillus licheniformis* GSTs are selected from the group consisting of SEQ ID NOs. 1-4448, nucleic acid fragments of SEQ ID NOs. 1-4448, and nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

49. The computer-based system of claim 47, wherein the *Bacillus licheniformis* GSTs

are SEQ ID NOs. 1-4448.

50. The computer-based system of claim 47, wherein the *Bacillus licheniformis* GSTs are nucleic acid fragments of SEQ ID NOs. 1-4448.

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51. The computer-based system of claim 47, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

52. The computer-based system of claim 51, wherein the *Bacillus licheniformis* GSTs 10 are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-4448.

53. The computer-based system of claim 52, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 1-4448.

15 54. The computer-based system of claim 45, wherein the *Bacillus* GSTs are *Bacillus clausii* GSTs.

55. The computer-based system of claim 54, wherein the *Bacillus clausii* GSTs are selected from the group consisting of SEQ ID NOs. 4449-8481, nucleic acid fragments of 20 SEQ ID NOs. 4449-8481, and nucleic acid sequences having at least 85% homology to the sequences of SEQ ID NOs. 4449-8481.

56. The computer-based system of claim 54, wherein the *Bacillus clausii* GSTs are SEQ ID NOs. 4449-8481.

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57. The computer-based system of claim 54, wherein the *Bacillus clausii* GSTs are nucleic acid fragments of SEQ ID NOs. 4449-8481.

58. The computer-based system of claim 54, wherein the *Bacillus clausii* GSTs are 30 nucleic acid sequences having at least 85% homology to SEQ ID NOs. 4449-8481.

59. The computer-based system of claim 58, wherein the *Bacillus clausii* GSTs are

nucleic acid sequences having at least 90% homology to SEQ ID NOs. 4449-8481.

60. The computer-based system of claim 59, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 4449-8481.

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61. The computer-based system of any of claims 45-60, wherein the *Bacillus* cells are selected from the group consisting of a *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lenthus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, and *Bacillus thuringiensis* cell.

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62. The computer-based system of any of claims 45-60, wherein the *Bacillus* cells are the same cell.

15 63. The computer-based system of any of claims 45-60, wherein the first *Bacillus* cell is a *Bacillus licheniformis* or *Bacillus clausii* cell.

64. The computer-based system of claim 63, wherein the *Bacillus licheniformis* cells are *Bacillus licheniformis* ATCC 14580 cells.

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65. The computer-based system of claim 63, wherein the *Bacillus clausii* cells are *Bacillus clausii* NCIB 10309 cells.

25 66. The computer-based system of any of claims 45-60, wherein the one or more second *Bacillus* cells are *Bacillus licheniformis* or *Bacillus clausii* cells.

67. The computer-based system of claim 66, wherein the *Bacillus licheniformis* cells are *Bacillus licheniformis* ATCC 14580 cells.

30 68. The computer-based system of claim 66, wherein the *Bacillus clausii* cells are *Bacillus clausii* NCIB 10309 cells.

69. The computer-based system of any of claims 45-60, wherein the *Bacillus* cells are one or more different cells.

70. A substrate comprising an array of *Bacillus* GSTs.

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71. The substrate of claim 70, wherein the *Bacillus* GSTs are selected from the group consisting of *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* GSTs.

10 72. The substrate of claim 70, wherein the *Bacillus* GSTs are *Bacillus licheniformis* GSTs.

15 73. The substrate of claim 72, wherein the *Bacillus licheniformis* GSTs are selected from the group consisting of SEQ ID NOs. 1-4448, nucleic acid fragments of SEQ ID NOs. 1-4448, and nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

20 74. The substrate of claim 72, wherein the *Bacillus licheniformis* GSTs are SEQ ID NOs. 1-4448.

25 75. The substrate of claim 72, wherein the *Bacillus licheniformis* GSTs are nucleic acid fragments of SEQ ID NOs. 1-4448.

76. The substrate of claim 72, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 85% homology to SEQ ID NOs. 1-4448.

30 77. The substrate of claim 76, wherein the *Bacillus licheniformis* GSTs are nucleic acid sequences having at least 90% homology to SEQ ID NOs. 1-4448.

78. The substrate of claim 77, wherein the *Bacillus licheniformis* GSTs are nucleic

acid sequences having at least 95% homology to SEQ ID NOs. 1-4448.

79. The substrate of claim 70, wherein the *Bacillus* GSTs are *Bacillus clausii* GSTs.

5 80. The substrate of claim 79, wherein the *Bacillus clausii* GSTs are selected from the group consisting of SEQ ID NOs. 4449-8481, nucleic acid fragments of SEQ ID NOs. 4449-8481, and nucleic acid sequences having at least 85% homology to SEQ ID NOs. 4449-8481.

10 81. The substrate of claim 79, wherein the *Bacillus clausii* GSTs are SEQ ID NOs. 4449-8481.

82. The substrate of claim 79, wherein the *Bacillus clausii* GSTs are nucleic acid fragments of SEQ ID NOs. 4449-8481.

15 83. The substrate of claim 79, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 85% homology to SEQ ID NOs. 4449-8481.

84. The substrate of claim 83, wherein the *Bacillus clausii* GSTs are nucleic acid 20 sequences having at least 90% homology to SEQ ID NOs. 4449-8481.

85. The substrate of claim 84, wherein the *Bacillus clausii* GSTs are nucleic acid sequences having at least 95% homology to SEQ ID NOs. 4449-8481.

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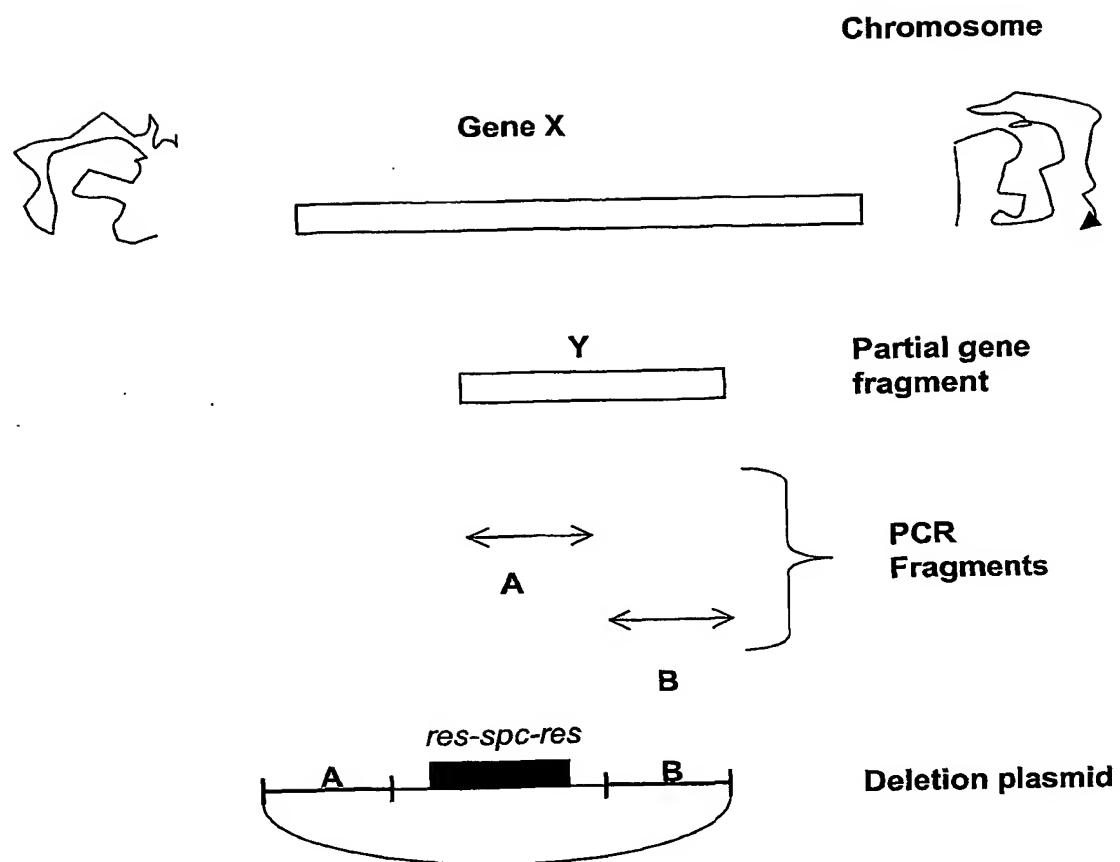


Fig. 1